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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  420
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  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1202
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   US-10-437-963-20266
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US-10-425-114-229
US-10-425-115-18957
US-10-425-115-18957
US-10-425-115-18957
US-10-425-114-14357
US-10-425-114-24903
US-10-425-114-24903
US-10-425-114-24903
US-10-425-115-38025
US-10-412-699B-1060
US-10-425-115-38025
US-10-425-115-38025
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US-10-425-115-3805-566
US-10-374-780A-566
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Biocceleration Ltd.
Sequence 20266, A
Sequence 3220, Ap
Sequence 568, App
Sequence 1061, Ap
Sequence 1158957, A
Sequence 14357, A
Sequence 1057, Ap
Sequence 24903, A
Sequence 567, App
Sequence 567, App
Sequence 30025, A
Sequence 1060, Ap
Sequence 30025, A
Sequence 30025, A
Sequence 30025, A
Sequence 366, App
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Sequence 368, App
Sequence 368, App
Sequence 37, App11
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equence 25, App	equence 1637, A	e 1543, A	15772,	31390,	84195,	Sequence 39218, A	55050,	68443,	9 7945, F	1636, F	1542, 7	20587	37,	37, App	531	27081,	056,	563, Ap		equence 15127	e 117	equence 1058,	565,	ce 2563	equence 11055,	equence 90448,	Sequence 3, Appli

## ALIGNMENTS

US-10-437-963-20266

Sequence 20266, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas APPLICANT: Kovalic, David APPLICANT: Zhou, Yihua

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APPLICANT: Kovall, ...
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
ping
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US-10-437-963-20266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 20266
LENGTH: 1228
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
FILE REFERENCE: 10 NOT NET NET ASSOCIATED TO SECTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1202; Best Local Similarity 100.0%; Pred. No. 0; Matches 1202; Conservative 0; Mismatches
121 GGTCCATGGACGCCGGAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCAC 180
                                                                                                                                                                           61 AGGGAAGGAGCAAGCACAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAG
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RESULT 3
US-10-425-114-3220
; Sequence 3220, Application US/10425114
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Sequence 6995, Application US/10487901
; Sequence 6995, Application No. US20050091708A1
; Publication No. US20050091708A1
; PublicANT: Nordendo, Jeremiah Vincent
APPLICANT: McCrery, David
; APPLICANT: McCrery, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Miller, Bath
APPLICANT: Blakeslee, Beth
APPLICANT: Blakeslee, Beth
APPLICANT: Larrinua, Ignacio
APPLICANT: Reddy, Avutu
APPLICANT: Reddy, Avutu
APPLICANT: Crosley, Rodney
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
FILE REFERENCE: DOW-08552
CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6995
LENGTH: 454
TYPE: DNA
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US-10-487-901-6995
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US-10-487-901-6995
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Best Local Simi
Matches 423;
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CGCCTCGA
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                                                                                                                                               GAGGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCC
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                             428
 454
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Pred. No. 2.1e-111;
0; Mismatches 5;
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313)8
CCURRENT APPLICATION UNMBER: US/10/425,114
CURRENT APPLICATION UNMBER: US/10/425,114
CURRENT APPLICATION UNMBER: US/10/425,114
CURRENT APPLICATION UNMBER: US/10/425,114
CURRENT APPLICATION UNMBER: US/10/425,114
COURTENT OF SEQ ID NOS: 73128
SEQ ID NO 3220
LENGTH: 1276
TYPE: DNA
ORGANISM: Zea may8
FEATURE:
OTHER INFORMATION: Clone ID: 700243864_FLI
US-10-425-114-3220
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Best Local Similarity
Matches 711; Conserv
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 GAGACGCTGTCCATGCCGCTGGACAGCTTCGACGACGTCCCCACGGAGCCCTGCAGCTCC
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Pred. No. 3.7e-98;
0; Mismatches 308;
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APPLICANT: YU, GUO-LIANG
FILE REFERENCE: MBI-O047 CIP
FILE REFERENCE: MBI-O047 CIP
CURRENT APPLICATION WINDER: US/10/374,780A
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/336,049
PRIOR APPLICATION NUMBER: 09/336,692
PRIOR APPLICATION NUMBER: 00/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/338,692
PRIOR FILING DATE: 2002-11/1,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR APPLICATION NUMBER: 10/225,067
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PRIOR APPLICATION NUMBER: 10/225,067
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09 GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K Sequence 568, Appublication No. APPLICANT:
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APPLICANT: Riechmann, Jose Luis Jiang, Cai-Zhong Heard, Jacqueline E Haake, Volker Reuber, T. Lynne Keddie, James Broun, Pierre E Pilgrim, Marsha L Dubell III, Arnold Pineda, Omaira Adam, Luc J Ratcliffe, Oliver Creelman, Robert A Application US/10374780A o. US20040019927A1

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Best Local S
Matches 711
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SEQ ID NO 568
LENGTH: 1352
TYPE: DNA
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APPLICANT: Dubell, Arnold N.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynuclectides and Polypeptides in PILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,032
PRIOR APPLICATION NUMBER: 09/533,032
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-27
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US-10-412-699B-1061
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                   SOFTWARE: PatentIn v
SEQ ID NO 1061
LENGTH: 1352
TYPE: DNA
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APPLICANT: Mendel Biotechnology, Inc. Applicant: Zhang, James
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                                                                                                                             Remaining Prior Application data NUMBER OF SEQ ID NOS: 2011
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ORGANISM: Zea mays
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Yu, Guo-Liang
Yu, Guo-Liang
Jiang, Cai-Zhong
Samaha, Raymond R.
Pilgrim, Marsha L.
Creelman, Robert A.
DuBell, Arnold N.
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Adam, Luc J.
Broun, Pierre E.
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                                                     GTTTAGAGCGCGCACGCGCGCGCGAGAATTTTCAGTTCCCTGGCTAATTGATTCATCGTT
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                                                                                               ATCTAGAG-----AAAGAGAGAGAATTTTACCGTTTCTTCGGTTAATTGAT---TTGTT
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                                                                                                                                         ATGGACTACTGGCTCGGAGTGTTCATGGAGTCCGGCGAAGCG----CAAGACTTGCCGCAG
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TAATTAATAGAGGGGTGTGTGTTGAGGACCACGACGAGATTAGGAAGAAACAACGCGA
                   TGAGCGAATCATCAAGCAGGAAGAACGCGAATCATGCGATGCGATGCGATGAGATGCACC
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GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITIE OF INVENTION: Nucleic acid Molecules a

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 158957

LENGTH: 1352.

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

FEATURE:

TYPES INFORMATION: Close ID NOTICE 2003-04-28

ORGANISM: Zea mays
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Best Local Similarity
Matches 714; Conserv
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                                                                                                                                                                                                                                                   437
                                                                                                                                                                                                                                                                                                                      256 TACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGAGGACACCATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                      257
                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GAGGAGGACAAGGTCCTCGTCGCCCCACATCCAGCGCCACGGCCACGGCCACCTGGCGCCC
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GGCGGAGGAGCACGCCAACGCCGGGATCAGCTCCGCGTCCGTGTGCGCCCAAGGA
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                                        GGCGTCGCCCGAGCGGTCCGCCTCGTCGGTGACGGAGTCCTCGATGGCCTCGTCGGT
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                          CACCACCGCGCGGCGTCGCCTGAACGGTCGGCGGCCTCGTCGTCGTCGTGACCGAGTCGAC
                                                                                ACCAAGCAGCTGGAGCAGGAGCAGCÁCGGGGGGCGCÁTGCAGGTGGTGACGCCGGCÁGGÁÁG
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ilarity 65.0%;
Conservative
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Pred. No. 3.2e-97;
0; Mismatches 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1352;
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14357
LENGTH: 1280
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
CTHER INFORMATION: Clone ID: LIB189-026-F3_FLI
US-10-425-114-14357
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US-10-425-114-14357
; Sequence 14357, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 706; Conser
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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                                                                                    Score 366; DB 8;
Pred. No. 1.8e-95;
0; Mismatches 270;
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RESULT 8
US-10-374-780A-564
; Sequence 564, Application US/10374780A
; Publication No. US2004001927A1
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Hand, Jac.,
Hanke, Volker
Creelman, Robert
Creer
AMT: Reuber, T. Lynne
AMT: Reber, T. Lynne
AMT: Broun, Pierre
Lant: Piligrin, Marsha L
CANT: Piligrin, Marsha L
PRIOR PILIGRIN, Marsha L
PRIOR APPLICATION NUMBER: 60/316,049
PRIOR APPLICATION NUMBER: 10/215,066
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR PILING DATE: 2002-08-09
VUMBER OF SEQ ID NOS: 2906

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APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose L
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline
APPLICANT: Haake, Volker
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                                                                 CCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGA
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GGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAG
                                                                                                                                   CAACTGGCGCGCGCTGCCCAAGCAAGCCGGCTTGCTGCGGTGCGGCAAGAGCTGCCGGCT
                                                                                                                                                            CAACTGGCGCCCCTGCCCAAGCAAGCCGGGCTGCTGCTGCGTTGCGGCAAGAGCTGCCGGCT
                                          CCGGTGGATCAACTACCTGCGCCCGGACATCAAGCGCGGCAACTTCAGCAAGGAGGAGGA
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
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Sequence 1057, Application US/10412699B Publication No. US20040045049A1 GENERAL INFORMATION:
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APPLICANT: Zhang, James
APPLICANT: Fromm, Michael E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Riechmann, Jose Luis
Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
Yu, Guo-Liang
Jiang, Cai-Zhong
Samaha, Raymond R.
Pilgrim, Marsha L.
Creelman, Robert A.
DuBell, Arnold N.
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Adam, Luc J.
Broun, Pierre E.
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US-10-412-699B-1057
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NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1057
LENGTH: 1344
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Best Local Similarity
Matches 706; Conserv
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
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CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-11-16
APPLICATION NUMBER: 09/819,142
FILING DATE: 2001-03-27
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APPLICATION NUMBER: 09/533,029
FILING DATE: 2000-03-22
APPLICATION NUMBER: 09/532,591
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FILING DATE: 2000-02-17
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Pred. No. 1.8e-95;
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 24903
LENCTH. 1126
                                                             Query Match
Best Local S
Matches 683
                                                                                                                                                                                                                                                                                                                                                               Sequence 24903, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                           FEATURE:
                                                                                                                                                                                                          ENGTH: 1126
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                                                                            Similarity
                  ACAATGGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCG
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                                                             29.3%;
llarity 66.8%;
Conservative
                                                                                                                                       Clone ID: LIB3732-032-B8_FLI
                                                             Score 352.6; DB 8;
Pred. No. 1.3e-91;
); Mismatches 224;
                                                                                           Length 1126;
                                                              116;
                                                              Gaps
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RESULT 11
US-10-374-780A-567
; Sequence 567, Application US/10374780A
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APPLICANT: Haang, Cai-Zhong
APPLICANT: Haang, Colker
APPLICANT: Adam, Luc J
APPLICANT: Applicant: Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Number: 105/10/374,780A
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/3310,847
PRIOR APPLICATION NUMBER: 60/3310,847
PRIOR APPLICATION NUMBER: 60/3310,847
PRIOR APPLICATION NUMBER: 60/336,49
PRIOR APPLICATION NUMBER: 60/336,49
PRIOR APPLICATION NUMBER: 60/336,692
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PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
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Local Similarity 66.8%;
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      376 ACGGACAACGAGATCAAGAACGTGTGGCACACCCCACCTCAAGAAGCGCCTCGATGC----
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                                          AGCCTCCACGAGCAGCTCGGCAACAGGTGGTCCGCCATCGCCGCCAGGCTGCCCGGGCGG
                                                                 CATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGAGG
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Pred. No. 1.5e-91
0; Mismatches 22
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RESULT 12
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APPLICANT:
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APPLICANT: Zhang, James
APPLICANT: Fromm, Michael E.
APPLICANT: Heard, Jacqueline E.
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Jiang, Cai-Zhong
Samaha, Raymond R.
Pilgrim, Marsha L.
Creelman, Robert A.
DuBell, Arnold N.
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Broun, Pierre E.
Pineda, Omaira
Reuber, T. Lynne
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Fromm, Michael E.
Heard, Jacqueline E.
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PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR TILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR PILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR PILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 09/531,944
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-13-27
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
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PRIOR FILING DATE: 2000-11-16
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NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1060
LENGTH: 1492
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Best Local Similarity
Matches 683; Conserv
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APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucieotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
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Pred. No. 1.5e-91;
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US-10-425-115-39025
J Sequence 39025, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 39025
LENGTH: 815
TYPE: NUM
                                                                                                Query Match
Best Local Similarity
                                                                                                                                     OTHER INFORMATION: Clone ID: MRT4577_135592C.1
-10-425-115-39025
                                                                                                                                                            ORGANISM: Zea mays FEATURE:
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AGAGGGAGAGGAGCGGTAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGCCTCAAGAGG
                                                     AGGGAAGGAGCAAGCACAATGGGGAGGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAA 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGAGGAGTTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTCGGCGTCCGCGTCTCGTGTGCGCCAAGGAGGAGAG-----CTCCTTCACCTCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCACCGGAGGGACATAGCTAACAGACAAGAGTGTCCATGAGCGAATCATCAAGCAGGAA 979
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                                                                                      Conservative
                                                                                                28.8%;
                                                                                     0,
                                                                                     Score 345.6; DB 9;
Pred. No. 1.3e-89;
0; Mismatches 189;
                                                                                     Indels
                                                                                                             Length
                                                                                                             815;
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                                                                                     Gaps
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US-10-425-115-38157
; Sequence 38157, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: MRT4577_134802C.1 US-10-425-115-38157
                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated |
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)|
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 38157
LENGTH: 1400
TYPE: DNA
TYPE: DNA
                                                                                                                                                                            Query Match 28.8%;
Best Local Similarity 70.5%;
Matches 550; Conservative
                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
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                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CTCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 ACCTCGGCTTCCGAGGAGTTCCAGATCGACGACAGCTTCTGGTCGGAG 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 GGCAACGCCGGGATCAGCTCGGCGTCCGCGTCCGTGTGCGCCCAAGGAGGAGAGCTCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 AAGCCGGCGGCGGCGCGCAAGCGCGAGGGCAAGATCAAGATGAGGAAGCTCGACGCG
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                                                                                                                               76 ACAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCG 135
                            GAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCC
                                                                                     TAATGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTGAAGAAGGGGCCATGGACGCCC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGTCCGCCTCCGCGTCCAAGGAGGAGTGCTTCACCTCGTCCAAG
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                                                                                                                                                                                 0
                                                                                                                                                                            Score 345.6; DB 9;
Pred. No. 1.6e-89;
0; Mismatches 164;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                       Length 1400;
                                                                                                                                                                                 66;
                                                                                                                                                                                 Gaps
236
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RESULT 15
US-10-374-780A-566
; Sequence 566, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
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                                                                                                                                                                       APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jacqueline E
APPLICANT: Creelman, Robert A
APPLICANT: Creeliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marbha L
APPLICANT: Pilgrim, Marbha L
APPLICANT: YU, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,847
                                                                                                                                         APPLICANT:
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                                                                                                                                      Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
Reuber, T. Lynne
Keddie, James
Broun, Pierre
Erilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
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PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-06-14
PRIOR PPLIOR DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR APPLICATION NUMBER: 10/225,067
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NUMBER OF SEQ ID NOS: 2906
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LENGTH: 1084
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                       TACCAGATCGACGACAGCTTCTGGTCCGAGACGCTGGCGATGACGACGACGGTGGACAGC
                                          TTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGACGGGTACGAC
                                                                                           TACTCGGCCGCCTCGTCGCTGGAGAACGCGGGCGACAGCTTCACGTCGGAGGAGGACTAC
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		Search completed: June 25, 2006, 09:58:37 Job time : 1548 secs	leted:	Search completed: Ju Job time : 1548 secs	ci s
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           pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: KEMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfiles1.seq:*
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Sequence 2027, Ap
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Sequence 1765,	Sequence 1, Appli	•	•	•	Sequence 502, Ap	Sequence 494, Ap	Sequence 1823, Ap			Sequence 521, Ap	Sequence 2045, A	-	Sequence 2041, Ap	Sequence 93, Appl	Sequence 282, Ap	Sequence 2074, Ap	•	Sequence 2085, A	•	Sequence 1935, A	Tradition 't company

ALIGNMENTS

## APPLICANT: Wood, Marion APPLICANT: Shenk, Michael A. APPLICANT: Shenk, Michael A. APPLICANT: Shenk, Annette APPLICANT: Glenn, Matthew ITILE OF INVENTION: Compositions and Methods for the ITILE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2027 LENGTH: 786 TYPE: DNA 밁 á 밁 5 밁 ; ORGANISM: Eucalyptus grandis US-09-640-211A-2027 US-09-640-211A-2027 Query Match Best Local S Matches 271 Sequence 2027, Application Patent No. 6833446 GENERAL INFORMATION: Local Similarity 70.( les 271; Conservative 360 167 300 AGCACATGAACAAAGGGGCATGGAGCAAGGAGGACGAGCGCCTCATCGCCTACATCA 107 240 47 TGGGGCTCAAGAAGGGTCCATGGACGCCGGAGGAGGAGACAAGGTCCTCGTCGCCCACATCC GTTGGGAAAAAGGATAAAGGCAGGAGAAGGAGGATGGGGAGGTCACCGTGTTGCGAGAGCG GTTCAGATCAGAGCAGGAAGGAAGCACAATGGGGAGGGCTCCGTGCTGCGAGAAGA AGCGCCACGGCGAAGGCTGCTGGCGATCCCTTCCAAAAGCAGCCGGCCTGCTGCGCCTGCG 16.8%; US/09640211A Score 201.4; DB 3; Pred. No. 3.1e-33; 0; Mismatches 116; Length Indels 786; 0;

Gaps

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GCAAGAGCTGCCGGCTCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACT

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TCTCCAAGGAGGAGGAGGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGT 346

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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
ITITLE OF INVENTION: Compositions and Methods for the
ITITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2036
LENOTH: 648
                                                                                                                                                                                               RESULT 3
US-08-722-626B-1
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US-09-640-211A-2036
Sequence 2036, Application US/09640211A
Patent No. 6833446
           Sequence 1, Application US/08722626B

Sequence 1, Application US/08722626B

Patent NO. 5939601

GENERAL INFORMATION:
APPLICANT: Klessig, Vinong
APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF ENQUENCES: 9

CORRESPONDENCE ADDRESS: ADDRESSE: Dann, Dorfman, Herrell and Skillman
ADDRESSE: Dann, Dorfman, Herrell and Skillman
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Best Local Similarity
Matches 255; Conserv
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1601 Market Street
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Pred. No. 6.5e-33;
D; Mismatches 92;
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STATE: I
COUNTRY:
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; NAME/KEY: Coding Sequence
; LOCATION: 148...981
; OTHER INFORMATION:
US-08-722-626B-1
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Best Local Similarity 71.6%;
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4004
TELEFAX: 215 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1344 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 27-SEP-1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 AAAGAAAATGGTGAGAGCTCCTTGTTGTGAGAAAATGGGGCCTGAAAAAAAGGGCCATGGAT
                                                                                                                                                                                                                                                                                                                       CGCCCTGCCCAAGCAAGCCGGGCTGCTGCCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGAT 251
                                                                                                                                                                                                                                                                                                                                                                                            TCCTGAAGAACATCAGATTCTCATCTCTTTCATTCAAACTAATGGCCATGGCAACTGGCG
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                                           CATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGG
                                                                                                                                                                                                                                           CAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCAT
ACGAACAGACAATGAAATAAAAATGTTTGGCACACCCACTTGAAGAAGAAGCTCAAAG
                                                                                             TATCCAGTTACATGAAATGCTTGGCAATAGATGGTCTGCAATAGCAGCAAAATTACCAGG
                                                                                                                                                                                           AGCCCTTCCCAAACAGGCTGGACTATTGAGATGCGGGAAGAGTTGCAGACTGCGGTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 195.8; DB 2;
Pred. No. 5.3e-32;
0; Mismatches 102;
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Gaps

191

260

200

RESULT 4 US-09-533-029-61 ; Sequence 61, Application US/09533029

499 430

440 371 380 311

320

GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre

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APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heaber, Lynne
FIILE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-Olo
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 61
T.ENGTH. 1046
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GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
                                                                                                                                                                                      Sequence 1965, Application US/09640211A Patent No. 6833446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 253; Conserv
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APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGGAAGAGCTCCATGCTGTGAGAAGATGGGGTTGAAGAGAGGACCATGGACACCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGAGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATCAAATCTTGGTCTCTTTTATCCTCAACCATGGACATAGTAACTGGCGAGCCCTC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
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APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: McGrath, Annette

APPLICANT: McGrath, Annette

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 252

LENGTH: 563
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                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Eucalyptus US-09-640-211A-252
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; ORGANISM: Eucalyptus
US-09-640-211A-1965
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for W
SEQ ID'NO 1965
LENGTH 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 252, Application Patent No. 6833446
                                                                                                       Query Match 16.0
Best Local Similarity 72.0
Matches 263; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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115 AAGAAGGGTCCATGGACGCCGGAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCAC 174
                                   193 CAGAGGGTCGCGCGCGCACGAGACATGGGACGATCCCCTTGCTGCGAGAAGGCGCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 AAGCGCCTCGATGCGCCGG 436
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                                                                  55 CAGAGCAGGGAAGGAAGCACAATGGGGAAGGCTCCGTGCTGCGAGAAGATGGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 AAAGGGCCGTGGACGGCGGAGGAGGACCGGAAGCTGGTCAACTTCATACTCACCCACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGAAAGCCTGGTTATCGATCTCCATGCCACTCTCGGCAATAGGTGGTCCAAAATAGCA
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                                                                                                    16.0%; Score 192.6; DB 72.5%; Pred. No. 2.1e-31 tive 0; Mismatches 9
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69.4%;
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Pred. No. 1.3e-31;
0; Mismatches 116;
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
ITILE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FFASESEQ for Windows Version 4.0
SEQ ID NO 1266
LENGTH: 360
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1266
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US-09-640-211A-1266
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wood, Marion APPLICANT: Shenk, Micha
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
   302
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                                                                                                                                                                                                                                                                      128 GGACGCCGGAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACT 187
                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                       68 GAGCAAGCACAATGGGGAGAGGGCTCCGTGCCGAGAAGATGGGGCTCAAGAAGATCGAT
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CCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGC 367
                                                                                                                     GGATAÑACTACCTCCGCCCCGACCTCAÑ-CGCGGCAACTTCACCGAGGAAGAAGACGAGC 241
                                                                                                                                       GGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAGGAGGACA
                                                                                                                                                                                                    GGCGCGCCCTGCCCAAGCAAGCCGGGCTGCTGCCTTGCGGCAAGAGCTGCCGGCTCCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCACGGCAACTGGCGCGCCCTGCCCAAGCAAGCCGGGCTGCCTTGCGTTGCGGCAAGAGC
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                                                           TCATCATCAAGCTCCACAGCTTGCTCGGCAACAAGTGGTCTCTGATCGCGGGGAGATTGC
                                                                                                                                                                                 GGCGCTCCCCCAAATCTGCCGGGCTTCTCAGGTGCGGCAAGAGCTGCAGGCTCAGGT 182
                                                                                                                                                                                                                                          GGACCAAGGAAGAGGACCAGCGCCTCATCGACTACATCCGCCTCCACGGCGAAGGTTGCT 122
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                                                                                                                                                                                                                                                                                                                                                                            Score 190.8; DB 3
Pred. No. 4.5e-31;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                            Length 360;
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APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: Shenk, Michael A.

APPLICANT: McGrath, Annette

APPLICANT: Glenn, Matthew

ITITE OF INVENTION: Compositions and Methods for the

ITITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 1100.1021CIU

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 519

LENGTH: 513

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Pinus
US-09-640-211A-519
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US-09-640-211A-519
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Best Local
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371
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                        GGACGGACAACGAGATCAAGAACGTGTGGCACACCCACCTCAAGAAGCGCCTCG
                                                                                                          TCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGA
                                                                                                                                                                                                                                                                                             CCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCA
                                                                                                                                                                                                                                                                                                                                     TAGACGAAGATAAAATACTCGTCGATTACATTACCAAACATGGCCATGGCAACTGGCGCG
GAACCGACAATGAGATCAAGAACGTGTGGAACACCCATTTAAAGAAACGTCTCG
                                                                             TTAAATTGCATGAGCTCATAGGGAATAGATGGTCCACTATTGCTTCGTACTTGCCAGGAA
                                                                                                                                                                                                         ACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCA
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Pred. No. 4.9e-31;
0; Mismatches 102;
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424
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718 US-09-640-211A-1718 Sequence 1718, Application Patent No. 6833446 GENERAL INFORMATION: LENGTH: 631 TYPE: DNA ORGANISM: Pinus US/09640211A

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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Annette
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 2088
LENGTH: 1150
TYPE: DNA
ORGANISM: Pinus radiata
US-09-640-211A-2088
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US-09-640-211A-2088
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local :
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                        CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGAGGACACCATCATCCAT 318
                                                                     CCCAAGCAAGCCGGGCTGCGTGCGGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
                                                                                                          GACAACGAGATCAAGAACGTGTGGCACACCCCACCTCAAGA
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Pred. No. 2e-30;
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Composition of Gene Transcription
FILE REFERENCE: 11000.1021C11
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2087
LENGTH: 473
TYPE: DNA
ORGANISM: Pinus radiata
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GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: INVENTION: Modification of Gene Transcripti
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
                                                                                                                                                                                      Sequence 2105, Application US/09640211A Patent No. 6833446
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Best Local Similarity
Matches 241; Conserv
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                                                                                                                                                                                                                                                                                                                   340
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Pred. No. 4.2e-29;
0; Mismatches 99;
                                         Gene Transcription
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE, FastSEQ for Windows Version 4.0
SEQ ID NO 2075
LENCTH: 636
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-2075
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US-09-640-211A-2075
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Matches
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NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2105
LENGTH: 1576
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2075, Application US/09640211A Patent No. 6833446
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wood, Marion
                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
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                                                          CCGGAGGAGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGC 192
                                                                                                          AGCACAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACG
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 GCCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATC
                                                                                            AGCACGAGCACGGCAACGCCATGCTGCAGCAAGGTGGGGATAAAGAGAGGCCCGTGGACG
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Pred. No. 5.4e-29;
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Pred. No. 5.4e-29;
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                                                                                                                                                     Mismatches 108;
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                                                                                                                                                                                   DB 3;
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               US-09-640-211A-1982

Sequence 1982, Application

Patent No. 6833446

; GENERAL INFORMATION:
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   APPLICANT: Wood, Marion
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CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 1797
LENGTH: 509
TYPE: DNA
ORGANISM: Pinus radiata
US-09-640-211A-1797
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US-09-640-211A-1797
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Best Local Similarity
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APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CIU
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                        GACAACGAGATCAAGAACGTGTGGCACACCCCACCTCAAGA 418
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  GACAACGAGATAAAGAACTACTGGAACACACACATCAAAA
                                                                                                     CTCCACGAGGTGGTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGAGGACG
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                                                                           CTGCGTCCCGATCTGAAGCGTGGAAGCTTCACCGAAGAAGAAGAAGACGAGCTCATCATCAAA
                                                                                                                                                                                             CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCATCCAT
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Pred. No. 9.2e-29;
0; Mismatches 100
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US/09640211A

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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOPTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 1982
LENGTH: 373
TYPE: DNA
ORGANISM: Pinus radiata
US-09-640-211A-1982
Search completed: June 24, 2006, 19:41:23 Job time : 467 secs
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                                                                              351
                                                                                                                379
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                                                                                                                                                                                                                                                                    259 CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAGGAGGAGGACACCATCATCCAT 318
                                                                                                                                                                                                                                                                                                            171
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                                                                                                                                                                                                                                                                                                                                                                                      139 GAGGACAAGGTCCTCGTCGCCGCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAACGAGATCAAGAACGTGTG 401
                                                                                                                                                                                                                              CTGCGTCCTGATCTGAAGCGTGGAAACTTCTCAGAAGAAGAAGAAGAACTCATCATCAAA 290
                                                                                                                                                                                                                                                                                                          CCCAAGGCCGCAGGGCTGATGCGCTGCGGGAAGAGCTGCAGGCTCCGATGGATAAACTAC 230
                                                                              GACAACGAGATAAAGAACTACTG 373
                                                                                                                                                                                CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCCGGGAGGACG
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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  774
608.4
586.2
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2: 995
3: 995
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Match
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Gapop 10.0 , Gapext 1.0
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12265.518 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-521-811-1
1202
  GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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9b_est9::*
9b_gs81:*
9b_gs81:*
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  В
    CL969261
AB118162
CK008102
CK008102
CF986244
CK014902
B1805305
CK014563
CK011009
CK990405
CC1261029
CC1966455
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CK008265
CI175768
CC1175768
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CL969261 OBIFCC018
AB118162 AB118162
CK008102 279537816
CF9986244 155327816
CK014002 323197816
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CK014563 327907816
CK011009 2977867816
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327.4	327.4	327.4	327.8	330.2	331	331.6	335	339.6	340.2	340.2	350	350.4	351	351.4	368.2	376.2	385.8	391	395.6	407.8	430	430.4	435	443	445.8	
			27.3	27.5	27.5	27.6	27.9	28.3	28.3	28.3	29.1	29.2	29.2	29.2	30.6	31.3	32.1	32.5	32.9	33.9	35.8	35.8	36.2	36.9	37.1	
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## ALIGNMENTS

Query Match Best Local : Matches 77:	ORIGIN	FEATURES source		JOURNAL COMMENT	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	RESULT 1 CL969261 LOCUS DEFINITION ACCESSION VERSION
Query Match 64.4%; Score 774; DB 13; Length 774; Best Local Similarity 100.0%; Pred. No. 1.3e-176; Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Cryza sativa (indica cultivar-group)" /mol_type="genomic DNA" /db_xref="taxon:39946" /clone_lib="Oryza sativa Express Library" /note="Oryza sativa exon trapped genomic sequences"	omics.org.cn ce. ualifiers	Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559	An analysis of transcriptional regulation of the fice genome and its comparison to Arabidopsis Unpublished (2004) Contact: Chen Chen	1 (bases 1 to 774)  Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Diao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice Genome and	GSS. Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaee; Oryza.	CL969261 774 bp DNA linear GSS 21-SEP-2004 OsIFCCO18187 Oryza sativa Express Library Oryza sativa (indica Cultivar-group) genomic, genomic survey sequence. CL969261 GI:52393152

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                                                Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 638)
1 (bases 1 to 638)
Fujiwara,S., Tanaka,N., Kaneda,T., Takayama,S., Che,F. and
Isogai, A.
Analysis of flagellin perception signaling rice immune system using cDNA microarray Unpublished (2004)
Contact: Fang-Sik Che
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5, Ikoma-shi, Takayama-chou, Nara 630-0101,
Tel: 81-743-72-5459
Fax: 81-743-72-5459
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Location/Qualifiers
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/cell_line="OC"
/clone_lib="ZAPII rice Oc cDNA"
/note="specimen voucher: Oc-MA-2002 (NAIST, Japan);
country: Japan; induced by incompatible N1141 strain
Acidovorax avenae"
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Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 621
POLYA=No.
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The Genomes of Oryza sativa: A History of Duplications
PLoS Biol. 3 (2), e38 (2005)
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Oryza sativa (indica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                TCGCGCCGCCATCCGCCGACGACATGGACTACTGGCTCGGAGTGTTCATGGAGTCCGGCG
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/cell_type="sterile"
/dev_stage="heading/flowering"
/clone_lib="Oryza sativa cv. PA64s panicle sterile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="PA648"
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Query Match Best Local Matches 58		urci S	TITLE JOURNAL PUBMED	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 4 CF986244 LOCUS DEFINITION	Qy 11 Db 6	Qy 106 Db 55	Oy 10	A 10	Qy 8
y Match 48.8%; Score 586.2; DB 5; Length 601; Local Similarity 99.5%; Pred. No. 4.7e-131; hes 588; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	/organism="Oryza sativa (indica cultivar-group)" /mol type="mRNA" /cultivar="LYP9" /db xref="taxon:39946" /tissue_type="whole plant" /dev_stage="tillering" /clone_lib="Oryza sativa cv. LYP9 tillering whole plant cDNA library"	Department Cs Department Cs Comics Institute ng Road, Hangzhou 310 56805886 56805884 snaegenomics.org.cn 41.3 Forward sequence stop: 601 setion/Qualifiers	Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X., Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Shi,G., Shi,J., Liu,J., Li,J., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,O., Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z., Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P., Wu,S., Bounds of Oryza sativa: A History of Duplications PLos Biol. 3 (2), e38 (2005)	CF986244.1 GI:58587936 CF986244.1 GI:58587936 EST.  Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermacophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.  1 (bases 1 to 601)e; Oryzeae; Oryza.  1 (bases 1 to 601)e; Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,	CF986244 601 bp mRNA linear EST 04-FEB-2005 15532rsicee_11417.yl Oryza sativa cv. LYP9 tillering whole plant cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA sequence.	127 ATCATCAGAA 1136           612 ATCATCAGAA 621	067 TAGAAACAGAAGATCAGTGATCGAAACCTGAGATCCTTTCTCACAATGTGCAAACTGG 1126 	.007 TGAGATGCACCCAGTAGCTTTGATAGTTAATTTTCTTTTTTTACCTCCTTCCT	947 AAGAGTGTCCATGAGCGAATCATCAAGCAGGAAGAACGCGAATCATGCGATGCGATGCGA 1006 	187 ATTGATTTGTTTTTTCTCTCTCTGCCGCCATCTTGCACCGGAGGGACATAGCTAACAGAC 946

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                       Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 31
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@qenc-
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The Genomes of Oryza sativa: A History of Duplications plos Biol. 3 (2), e38 (2005)
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Oryza sativa (indica cultivar-group)
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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S035C08 Stem library from Oryza
Sativa cDNA clone S035C08, mRNA
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/dev_stage="heading/flowering"
/clone_lib="Oryza sativa cv. PA64s
library"
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/cell_type="sterile"
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/mol_type="mRNA"
/cultivar="PA64s"
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Pred. No. 2.8e-130;
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551 540 491 480 431 420 371 360 311 300 251 240

stage) EST

02-OCT-2001 Oryza

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8 밁 5 밁 Ś 8 8

594

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Gaps

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191 180 131 120 71 sterile

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Contact: Haitao Dong, Debao Li Bioinfomatics and Gene Network Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 0086-571-86961525
Email: webmaster@estarray.org, |
Seq primer: M13 forward primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
                                                                                     TTCCTGTATGTATAGAAACAGAAGAGATCAGTGATCGAAACCTGAGATCCTTTCTCACAA 1114
                                                                                                                                              TAGCTAACAGACAAGAGTGTCCATGAGCGAATCATCAAGCAGGAAGAACGCGAATCATGC
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                                         TTTCTTCGGTTAATTGATTTGTTTTTTTCCTCTCTCTCGCCGCCATCTTGCACCGGAGGGACA
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           ACTTGCACGCTAAAAAAAAAAAAAAAAAA 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa"
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Pred. No. 6.2e-130;
O; Mismatches 14;
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249
                    258
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Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou
Tel: 86-571-56805886
Fax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                Email: zhouyan@genomics.org.
Seq primer: M13 Forward
High quality sequence stop:
POLYA=No.
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15685292
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CK014563
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CCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCATCCA
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="PA64s"
/db_xref="taxon:39946"
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

CB (bases 1 to 585)

Yu.J., Wang,J., Lin,W., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Li,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,O.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Wu,O.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,

Wu,S. and Liu,J.

The Genomes of Oryza sativa: A History of Duplications

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32790rsicef_4442.yl Oryza sativa cv. PA64s panicle sterile cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
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310008, China (indica

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library" PA64s panicle sterile

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Spermatodeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                           Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzho
Tel: 86-571-56805886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK011009 581 bp mRNA linear EST 04-FEB-2005 29726rsicef_8456.yl Oryza sativa cv. PA64s panicle sterile cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
                                                                                                                                                                                                                                                 Email: zhouyan@genomics.org.
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                    Contact: Yan Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CK011009.1
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                                                                                                                                                                                                                                    quality sequence stop:
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              47.2%;
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Score 567.4; DB 5;
Pred. No. 1.7e-126;
0; Mismatches 1;
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                                            CCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
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SOURCE ORGANISM JOURNAL 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Jaraki 81-29-838-7007 Collection and mapping of over rice full- length cDNA project Unpublished (2006) Contact: Shoshi Kikuchi Department of Molecular Genetic Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1. (bases 1 to 550) CI166609 Cryza sativa (japonica cultivar-group) shoot and callus cultivar sativa (japonica cultivar-group) shoot and callus cultivar-group) cDNA clone 031-M064R-D01 3', Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full lengt
URL:http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yaze CI166609 CI166609.1 Kikuchi, S. mRNA sequence. Expression GI:86526403 Genetics, 30,000 transcription from japonica rice Head of Laboratory full length cDNA Project units of. γď

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Query Match
Best Local Similarity
Matches 549; Conserv
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FAIS Genome Sequencing & Analysis Group: Očomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Očomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Očomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Očomo, Y., Iida, Y., Kodawahi, M., Kodawahi, M., Kodawahi, M., Kodawahi, M., Kodawahi, M., Maruda, H., Miura, J., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Kusuma, K., Kun, M., Kuyu, R., Sugano, S., Yokomizo, S., Yokomizo, S., Yokomizo, S., Yasoh, H., Kawai, J., Alasawa, K., Alayatsu, N., Hiramoto, K., Hara, A., Hashizume, M., Hayatsu, N., Hiramoto, K., Hara, A., Hashizume, M., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kutoh, H., Kawai, J., Konagawa, S., Kutoh, H., Kawai, J., Konagawa, S., Kutoh, H., Kawai, J., Konagawa, S., Saltoh, H., Sabaki, C., Sakai, K., Sakai, C., Sakai, K., Sakai, S., S
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnollophyta; Liliopsida;
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                  Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W., Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X., Zhang,Y., Li,R., Xu,Z., Li,S., Liu,J. Zhang,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J. Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q., Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z., Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 56
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Tel: 86-571-56805886
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Hangzhou Genomics Institute
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                                                                                                GGTCCATGGACGCCGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACAC
                      GGCAACTGGCGCCCTGCCCAAGCAAGCCCGGGCTGCCTTGCGGCAAGAGCTGCCGG
GGCAACTGGCGCGCCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGG
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/cultivar="LYP9"
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Email: skluchienias.affrc.go.jp
Email: skluchienias.affrc.go.jp/cDNA/
URL:http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
Fujimura,T., Tkeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Fujimura,T., Tkeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hashizume,W., Haysshida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Xojima,Y., Kondo,S., Konno,H., Kouda,M.,
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoshi Kikuchi
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                  2-1-2 Kannondai, Tsu
Tel: 81-29-838-7007
Fax: 81-29-838-7007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collection and mapping rice full- length cDNA Unpublished (2006)
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543
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/clone_lib="Oryza sativa (japonica cultivar-group)
and root of germinating seeds"
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clade; Ehrhartoideae; Oryzeae; Oryza.
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                   TGTCCATGAGCGAATCATCAAGCAGGAAGAACGCGAATCATGCGATGCGATGCGATGAGA
                                                                                                                                          TTTGTTTTTTCTCTCTCTGCCGCCATCTTGCACCGGAGGGACATAGCTAACAGACAAGAG
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/dev_stage="trefoil"
/clone_lib="Oryza_sativa_c"
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (indica cultivar-group)"
|mol type="mRNA"
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Pred. No. 1.8e-117;
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RESULT 13
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Best Local Similarity
Matches 526; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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544 bp mRNA linear EST 04-17600rsicee_15506.yl Oryza sativa cv. LYP9 tillering whole cDNA library Oryza sativa (indica cultivar-group) cDNA 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
CF988227
CF988227.1 GI:58589919
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Seq primer: M13 Forward
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Bioinformatics Department
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                                                                                              CAGGTTGCCCGGGAGGACGGACAACGAGATCAAGAACGTGTGGCACACCCCACCTCAAGAA
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                        GCGCCTCGATGCGCCGGCTCAGGGCCGGTCATGTCGCGGCCGAGCGGCGGCCAAGAAGCACAA 479
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                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:39946"
/tissue_type="whole plant"
/dev_stage="tillering"
/clone_lib="Oryza_sativa_cona_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="LYP9"
                                                                                                                                                                                                                                                   43.6%;
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No.51 Zhijiang Road, Hangzhou 3
Tel: 86-571-56805884
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 509
POLYA=No.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Lillopsida;
Clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 509)
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library Oryza Bativa (indica cultivar-group) cDNA 5', mRNA
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                                                         CGCCTCGATGCGCCGGCTCAGGGCGGTCATGTCGCGGCGAGCGGCGGCGAGAAGAAGCACAAG
                                                                                       GAGGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCC
                                                                                                                                                                                              CTCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAG
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                     AAGCCGAAGAGCGCGAA 497
                                                                                                                                     GAGGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCC
                                                                                                                                                                                 CTCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAG
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ilarity 100.0%;
Conservative
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Pred. No. 2e-109;
0; Mismatches 0
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REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS RESULT 15 CI175768 LOCUS JOURNAL COMMENT SOURCE ORGANISM DEFINITION sequence. CI175768 CI175768.1 Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project URL:http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Kikuchi, S.
Collection and mapping of over rice full- length cDNA project Unpublished (2006)
Contact: Shoshi Kikuchi Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, viridiplantae, Streptophyta; Er
Spermatophyta; Magnollophyta; Liliopsida;
clade, Ehrhartoideae; Oryzeae; Oryza. CI175768 Oryza sativa (japonica cultivar-group) supermix Oryza sativa (japonica cultivar-group) supermix Oryza sativa (japonica cultivar-group) cDNA clone 034-M012R-H01 3', mRNA 2-1-2 Kannondai, Ts Tel: 81-29-838-7007 Fax: 81-29-838-7007 National Institute Department of (bases 1 to 500) GI:86535562 Molecular Tsukuba, 유 Agrobiological Sciences Genetics, Ibaraki 30,000 transcription from japonica rice 305-8602, Head of. Embryophyta; Tracheophyta; a; Poales; Poaceae; BEP units Å, the

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FEATURES
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Best Local Similarity
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ireda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kurura, T., Ireda, R., Ishibiki, J., Lu, M., Masuda, H., Miura, J., Mizura, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizura, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizura, T., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Yoshimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Akhura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Arakawa, T., Kapasawa, J., Katoh, H., Kawai, J., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kondo, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Saaski, D., Sato, K., Shibata, K., Sakai, K., Sakazume, N., Sano, H., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
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/mol type="mRNA"
/culTivar="Nipponbare"
/db_xref="taxon:39947"
/clone="034-M012R-H01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="supermix"
/clone_Tib="Oryza sativa (japonica cultivar-group)
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100.0%; Pred. No. 1.9e-108;
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Search completed: June 25, 2006, 09:32:38 Job time : 5484 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Minimum DB
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Maximum Match 100%
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Perfect score:
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2001as:*
4: geneseqn2001as:*
5: geneseqn2002as:*
7: geneseqn2002as:*
9: geneseqn2003as:*
9: geneseqn2003as:*
10: geneseqn2003ds:
11: geneseqn2004as:
13: geneseqn2004as:
14: geneseqn2004as:
15: geneseqn2004bs:*
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES	
Result	Score	Query Match	Length	80	В	Description
٠ :	752.6	62.6	918	ا و	ADA48105	Ada48105 Rice gene
N	752.6	62.6	816	片	ACL26123	3 Rice
ω	744.6	61.9	774	8	ADA69954	Ada69954 Rice gene
4	744.6	61.9	774	ø	ADA48651	Rice
ហ	744.6	61.9	774	11	ACL30325	Acl30325 Rice abio
0	420	34.9	454	10	ADD16949	
7	420	34.9	454	10	ADK59612	Adk59612 Plant DNA
80	375.2	31.2	1276	13	ADO84500	-
9	375.2	31.2	1352	12	ADI42105	Plant
10	375.2	31.2	1352	12	ADO02648	Ado02648 Corn orth
11	366	30.4	1280	13	ADX31537	Adx31537 Plant ful
12	366	30.4	1344	12	ADI42101	Adi42101 Plant tra
13	366	30.4	1344	12	ADO02644	Ado02644 Corn orth
14	352.6	29.3	1126	13	ADX50163	Adx50163 Plant ful
15	352.6	29.3	1492	12	ADI42104	Adi42104 Plant tra
16	352.6	29.3	1492	12	ADO02647	Ado02647 Corn orth
17	331.2	27.6	1084	12	ADI42103	-
18	331.2	27.6	1084	12	ADO02646	Ado02646 Corn orth

The invention relates to a novel isolated polynucleotide comprising plant nucleotide sequence having an open reading frame that encodes

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Claim 1; SEQ ID NO 175; 299pp; English.

pathogen.

WPI; 2003-184052/18. P-PSDB; ADA48106.

Moughamer hu T;

New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant

Ada70309 Rice gene	ADA70309	œ	1107	19.5	234	45
Aac41294 Zea mays	AAC41294	w	477	19.5	234.2	44
Adj41904 Plant cDN	ADJ41904	12	664	19.5	234.6	43
Plant	ADX51623	13	1772	19.6	235.8	42
	ADT17583	13	1540	19.7	236.2	41
Aea26884 Stress to	AEA26884	14	966	20.1	241.2	40
Adj77726 cDNA enco	ADJ77726	12	1427	20.2	243	39
Acd07381 Rice Myb-	ACD07381	8	1427	20.2	243	38
Ado03224 Corn orth	ADO03224	12	1302	20.3	244.6	37
Adi43080 Plant tra	ADI43080	12	1302	20.3	244.6	36
Adx60547 Plant ful	ADX60547	13	1285	20.3	244.6	35
Ada69370 Rice gene	ADA69370	œ	1023	20.4	245.8	34
Ada69399 Rice gene	ADA69399	æ	834	22.4	268.8	33
Ado03223 Corn orth	ADO03223	12	777	22.6	271.8	32
Adi43079 Plant tra	ADI43079	12	777	22.6	271.8	31
Adh50133 Rice Myb-	ADH50133	12	577	23.2	278.8	30
Abt08129 Myb-relat	ABT08129	σ	577	23.2	278.8	29
Ada70307 Rice gene	ADA70307	œ	672	23.6	284.2	28
Ado02643 Rice orth	ADO02643	12	643	25.2	302.8	27
Adi42100 Plant tra	ADI42100	12	643	25.2	302.8	26
Adk56097 Plant DNA	ADK56097	10	335	25.6	307.8	25
Ado82450 Plant ful	ADO82450	13	1086	26.0	312.6	24
Ado02645 Corn orth	ADO02645	12	662	26.1	314.2	23
Adi42102 Plant tra	ADI42102	12	662	26.1	314.2	22
Aac51733 Zea mays	AAC51733	w	1083	26.3	315.6	21
Adh50099 Rice Myb-	ADH50099	12	1074	27.2	326.6	20
Abt08112 Myb-relat	ABT08112 ·	თ	1074	27.2	326.6	19

## ALIGNMENTS

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RESULT 1
ADA48105
ID ADA4
XX ADA4
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XX ADA4
XX ADA5
AC AISE
XX Gise
XX Gise
XX WO20
XX WO20
XX Gise
PD 03-J
PR 22-J
PR 2
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Katagiri F, Kreps
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
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Kreps J, Provart N, Ricke D, Zhu
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Best Local Similarity
Matches 804; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a protein conferring disease resistance used in the invention.
              ACL26123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 816 BP; 164 A; 254 C; 280 G; 118 T; 0 U; 0 Other;
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                                                                                                 AGAGAAAGAGAGAGATTTTACCGTTTCTTCGGTTAA
                                                                                                                                                       TGGACTACTGGCTCGGAGTGTTCATGGAGTCCGGCGAAGCGCAAGACTTGCCGCAGATCT
                                                                                                                                                                                                                                                    CCGAGGAGTTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGACG
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               standard;
                                                                                                                                                                                               GGTACGACGTGTCCATGGAGCCCGGCGACGCGTTCGTCGCGCCGCCCATCCGCCGACGACA
                                                                                                                                                                                                               GGTACGACGTGTCCATGGAGCCCGGCGACGCGTTCGTCGCCGCCGCCCATCCCGCCGACCA
                                                                                                                                                                                                                                                                                                          GGATCAGCTCGGCGTCCGCGTCCGTGTGCGCCAAGGAGGAGAGCTCCTTCACCTCGGCTT
                                                                                                                                                                                                                                                                                                                          GGATCAGCTCGGCGTCCGCGTCCGTGTGCGCCAAGGAGAGAGCTCCTTCACCTCGGCTT
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                                                                                                                                       TGGACTACTGGCTCGGAGTGTTCATGGAGTCCGGCGAAGCGCAAGACTTGCCGCAGATCT
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               816
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Pred. No. 2.9e-139;
0; Mismatches 4;
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 804; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-2001;
26-SEP-2001;
21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
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Moughamer
                                                                                                                                                                                                                                                                                 Sequence 816 BP; 164 A; 254 C; 280 G; 118 T; 0 U; 0 Other;
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                                                      GAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCTG
                   CTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAGGAGGAGGACACCATCAT
                                                                                                               GAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCTG
                                                                                                                                                                                     ATGGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 79; 89pp; English.
CTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACCCATCAT
                                                                                                                                                                    ATGGGGAAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
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T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                       98.4%;
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N, Ricke
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                                                                                                                                                                                                                         Score 752.6; DB 11;
Pred. No. 2.9e-139;
0; Mismatches 4;
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D, Zhu T;
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CCATCTCCACGAGCTGCTTGGCAA----CAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGG

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AC ADA6
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                                                              Chang H,
Katagiri
Identifying at least pathogenic infection bacterial, fungal or
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                                                                                                                                                                                                                                Plant;
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                                                                                                                                     22-JUN-2001; 2001WO-IB001105
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                                                                                            SYNGENTA PARTICIPATIONS
                                                             Chen W, F, Quan
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S, Tao
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one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
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Whitham S, Xie
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.e Z,
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Best Local Sim
Matches 769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                       CTGGCTCGGAGTGTTCATGGAGTCCGGCGAAGCGCAAGACTTGCCGCAGATCTAG
                                                                GTTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGACGGGTACGA
                                                                                                        GTTCCAGATCGACGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGACGGGTACGA
                                                                                                                                      CTCGGCGTCCGCGTGTGCGCCAAGGAGGAGAGCTCCTTCACCTCGGCTTCCGAGGA
                                                                                                                                                 CTCGGCGTCCGCGTGTGCGCCAAGGAGGAGGAGCTCCTTCACCTCGGCTTCCGAGGA
                                                                                                                                                                              GGTGACGGAGTCCTCGATGGCCTCGTCGGTGGCGGAGGAGCACGGCAACGCCGGGATCAG
                                                                                                                                                                                         GGTGACGGAGTCCTCGATGGCCTCGTCGGTGGCGGAGGAGCACGGCAACGCCGGGATCAG
                                                                                                                                                                                                                       GAAGCCAGCCGCCGACGCCG-GCCGCCGGCGTCGCCGAGCGGTCCGCCTCGTCGTC
                                                                                                                                                                                                                                      TCAGGGCGGTCATGTCGCGGCGAGCGGCGCAAGAAGCACAAGAAGCCGAAGAGCGCGAA
                                                                                                                                                                                                                                                                                                                                                CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCCGGGAGGACG
                                                                                                                                                                                                                                                                                                                                                                                          CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                     CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCATCCAT
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Pred. No. 1.1e-137;
0; Mismatches 4;
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Best Local Similarity
Matches 769; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated polynucleotide comprising plant nucleotide sequence having an open reading frame that encodes polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance tolerance to a plant pathogen. The present sequence represents a gen conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide reading frame that resistance, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 721; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003000906-A2
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                                                                                                                                                                                                              CCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTTGCCGGCTCCGGTGGATCAACTAC
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                                                                                                                         CTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGACACCATCATCCAT
                                                                                                                                                                                                                                                                                                         GAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                          ATGGGGAAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                     ATGGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 BP; 150 A; 248 C; 269 G; 107
                             CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGAGGACG
                                                                                          CTGCGGCCGGACATCAAGCGGGCAACTTCTCCAAGGAGGAGGACACCATCATCCAT
                                                                                                                                                                                         CCCAAGCAAGCCGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
                                                                                                                                                                                                                                                                              GAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCCTG
  CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTCCCCGGGAGGACG
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(reps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising a plant nucleotide sequence having an open encodes a polypeptide associated with disease for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 744.6; DB 9; 
Pred. No. 1.1e-137; 
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tolerance; plant pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance
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hu T;
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                                                              New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0332179P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice abiotic
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T, Provart
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N, Ricke
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D, Zhu T;
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                                                                                       for altering the an abiotic stress
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                                                                                                                                          GTT CCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGACGGGTACGA
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                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polynucleotides described herein. This polynucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistancheat stress; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 454 BP; 111 A; 147 C; 141 G; 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid derived from Nicotiana benthamiana, sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crosley R,
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                                                                                                                                                                                                                                                                                                                                              Similarity
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DOW AGROSCIENCES LLC
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                                                                            AGGGAAGGAGCAAGCACAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAG
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                               Score 420; DB 10;
Pred. No. 1.6e-73;
0; Mismatches 5;
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The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered anino acid metabolism, altered ester metabolism, altered stered phenolic metabolism, altered carbohydrate metabolism, altered sterol, oxygenated terpene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alcohol metabolism; fatty acid metabolism;
branched fatty acid metabolism; alkaloid metabolism;
amino acid metabolism; ester metabolism; glyceride metabolism;
phenolic metabolism; carbohydrate metabolism; sterol metabolism;
terpene metabolism; isoprenoid metabolism; alkene metabolism;
alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                      Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and stero
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weglarz T,
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                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tole extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulatyield; plant growth; plant development; seed oil; protein yield;
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Pred. No. 1.6e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern, apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature sensecence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
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                                                                                                                                                                                   The invention describes a transgenic plant comprising a recombinant CC polynucleotide of any one of more than 500 nucleotide sequences fully CC defined in the specification or its complement. The method of the CC invention can be used to produced a plant having altered traits such as: CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone CC sensitivity; disease resistance; sugar sensing; early or late flowering; CC altered flower structure, change in stem bifurcations, altered branching cpattern, reduced apical dominance, reduced trichome density; lack of CC trichomes; reduced ectopic trichome development; altered branching cc increased root growth; increased root hairs; altered seem morphology; CC altered cell proliferation or cell differentiation; rapid development; CC altered cell proliferation or cell differentiation; rapid development; CC size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant CC anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in CC bioinformatic search methods. This sequence represents a plant CC transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.
                                                                                                                         Query Match
Best Local S
Matches 711
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Creelman RA,
Pilgrim ML,
                                                                                                                                                                  Sequence 1352
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAAK/)
(CREE/)
(RATC/)
(ADAM/)
(REUB/)
(KEDD/)
(KEDD/)
(BROU/)
(PILG/)
(DUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2003;
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(RIEC/)
(JIAN/)
(HEAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          more than
                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant comprising a recombinant more than 500 nucleotide sequences, useful
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CREEMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
                                                                                                                                     Similarity
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RIECHMANN J L.
                                         GAGGAGGACAAGATCCTGGTCGCGCACATCCAGAGCTTCGGCCACAGCAACTGGCGCGCG
                                                     GAGGAGGACAAGGTCCTCGTCGCCCACATCCAGGGCCACGGCCACGGCAACTGGCGCCCC
                                                                                  AGAATGGGGAGAGACTCCGTGCTGCCGAGAAGATGGGGCTCAAGAGGGGGCCATGGACGCCG
                                                                                               ACAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGAGGGTCCATGGACGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO
         CTGCCCAAGCAAGCCGGGCTGCGTGCGGGTAGAGCTGCCGGCTCCGGTGGATCAAC
CTGCCCAAGCAAGCCGGGCTGCTGCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAAC
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, Ratcliffe
Dubell AN,
                                                                                                                            Conservative
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                                                                                                                                                                    BP; 300
                                                                                                                                   31.2%;
                                                                                                                                                                  A; 431 C; 414
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Adam LJ,
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                                                                                                                         Score 375.2;
Pred. No. 1.4e
0; Mismatches
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Reuber TL,
'u G;
                                                                                                                           1.4e-64;
ches 308;
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                                                                                                                                                                    T; 0 U; 0 Other;
                                                                                                                                               DB 12; Length 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide of any one in bioinformatic search
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Keddie
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AD002648
ID AD002
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                                           standard;
  (first
                                           cDNA; 1352
  entry)
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TACCTGCGCCCGGACATCAAGCGCGGCAACTTCAGCAAGGAGGAGGACGCCATCATC
                                                                                                                                                                                                                                                                                                 TTTTCTCTCTCTGCCGCCATCTTGCACCGGAGGGACATAGCTAACAGACAAGAGTGTCCA
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GATATCGGTGATCGAAACCT
                            GAGATCAGTGATCGAAACCT 1097
                                                                                                                                                                                                                                                                   CTTTCTCTCTCCCCTGCACGTCTTGCAATCGGAATTCGGAGGGGACAGTCACAATAGCAGC
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                                                                                    TAATTAATAGAGGGGTGTGTGTGTGAGGACCACGACGAGATTAGGAAGAAACAACGCGA 1211
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22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
06-APR-2000;
 Claim 1;
                                                                          WPI; 2004-225755/21.
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(PILG/)
(CREE/)
(DUBE/)
(RATC/)
(KUMI/)
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14-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1999;
21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corn, transcription factor; es; gene; plant; transgenic; abiotic cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germ
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                                                                                                                                                                                    (SHER/
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                                              transgenic
                                                                                                   1 J,
1 O,
1 BK;
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                                                                                                                                                                              JIANG C.
SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMIMOTO R.
SHERMAN B K.
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ADAM L J.
BROUN P E.
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REUBER T L.
KEDDIE J S.
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                               FROMM
HEARD
SEQ ID NO 1062; 213pp; English
                               characteristics
                                                                                                                                   Fromm ME, |
Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00533392
2000US-00533488
2000WO-US009448
2000US-00713994
2001US-00837444
2001US-00837444
2002US-00958131
2002US-0025066
2002US-0025067
2002US-0025067
2002US-0025068
2002US-0025068
2002US-00374780
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2000US-00532591.
2000US-00533029.
2000US-00533030.
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                                              plant,
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                                                                                                                       Heard JE, Riechmann JL, Ac, Keddie JS, Yu G, Jiang (n RA, Dubell AN, Ratcliffe
                                            useful in developing
                               or traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant size; leaf morphology;
                                              phenotypes with altered
                                                                                                                  o, o
                                                                                                                                                      Adam
                                                                                                                       Samaha RS;
Kumimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
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The invention relates to a transgenic plant comprises a recombinant

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CATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCCGCCAGGTTGCCCCGGGAGG

375

374 315 ঠ

196

CTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAAC

CTGCCCAAGCAAGCCGGGCTGCTGCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAAC TACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGGAGGAGGACACCATCATC

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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 711; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genescence, lethality, increased necrosis, an increase in seeding or plant size, decreased plant size, a change in leaf morphology, increased altered leaf development, increased leaf size and mass, glossy leaves, leaf cell expansion, change in seed morphology, altered seed coloration, increased seed size, decreased size, altered seed shape, change in leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid content, increased leaf insoluble sugars, decreased leaf insoluble sugars, increased leaf anthocyanins, an alteration of leaf flucosinnolate content, change in seed biochemistry, an increase in seed oil content, increase in seed protein seed solutions, increase in seed seed oil content, increase in seed fatty acid content, increase in seed protein content, alteration in seed protein content, decrease in seed fatty acid content, alteration in seed protein content, decrease in seed protein secondary metabolism, increase in seed secondary metabolism, increase in seed protein secondary metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1352 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybear Rice, Rape or Corn, comprising any of the sequences appearing as ADO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in root anthocyanins, increase in plant anthocyanins, and alteration light response or shade avoidance. The present sequence encodes an
      255
                                                                     136
      GAGGAGGACAAGATCCTGGTCGCGCACATCCAGAGCTTCGGCCACAGCAACTGGCGCGCG
                                                               GAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCC
                                                                                                                                 AGAATGGGGAGAGCTCCGTGCTGCGAGAAGATGGGGGCTCAAGAGGGGGGCCATGGACGCCG
                                                                                                                                                                         ACAATGGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGTCCATGGACGCCG
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Pred. No. 1.4e
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plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                    Plant full
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                                                  length insert polynucleotide seqid 14357.
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                                                                             entry)
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Best Local S
Matches 706
                                                                                                                                                                                                                                                                                                                                                            plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                 Sequence 1280 BP;
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(KOVA/)
(SCRE/)
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05-NOV-2001;
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CAACTGGCGCGCCCTGCCCAAGCAAGCCGGGCTGCTGCCGTTGCCGGCAAGAGCTGCCGGCT
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                                    GCCATGGACGCCCGAGGAGACAAGGTCCTGGTCGCCCACATCCAGAGCTTCGGCCACAG
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Pred. No. 9.1e-63;
0; Mismatches 270;
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transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation;
                                                                            22-APR-2004
                                                                                                      ADI42101
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Best Loc Matches Query Match

Local

Similarity

30.4%; A;

Score 366; DB 12 Pred. No. 9.1e-63 0; Mismatches 27

270;

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Gaps

8

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Length 1344; Indels

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0 Other;

Conservative

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The invention describes a transgenic plant comprising a recombinant CC polynucleotide of any one of more than 500 nucleotide sequences fully CC defined in the specification or its complement. The method of the CC invention can be used to produced a plant having altered traits such as: CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone CC sensitivity; disease resistance; sugar sensing; early or late flowering; CC altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of CC trichomes; reduced ectopic trichome development; altered trichome CC development; increase in trichome number; altered seed development; company increase in trichome number; altered seed development; CC altered cell proliferation or cell differentiation; rapid development; CC altered cell proliferation or cell differentiation; rapid development; CC size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant CC transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transgenic plant methods. This sequence represents a plant crease in root anthocyanins; increase in the consistion of a transgenic plant with altered traits.
                                                                                                                                                                                                                                                                                                                                                                                                                       New transgenic
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(BROU/
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RATCLIFFE O.
ADAM L J.
REUBER T L.
REUBER T L.
REDUB J.
BROUN P E.
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PILGRIM M L.
DUBELL A N.
PINEDA O.
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Ratcliffe O, Adam LJ,
Dubell AN, Pineda O, Y
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22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
16-NOV-2000;
16-NOV-2000;
17-AFR-2001;
17-AFR-2001;
14-JUN-2002;
09-AUG-2002;
09-AUG-2002;
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                                                  Zhang J, Fr
Pineda O, R
Pilgrim ML,
Sherman BK;
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JIANG C.
SAMAHA R S.
PILCRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMLMOTO R.
SHERMAN B K.
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HEARD J E.
RIECHMANN I J.
ADAM L J.
BROUN P E.
PINEDA O.
REUBER T L
KEDDIE J S
YU G.
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FROMM
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Reuber TL,
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2000US-00533392
2000US-005339448
2000US-00713994
2000US-00713994
2001US-0087144
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                                                                            RA,
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                                                                         JE, Riechmann JL, Ao
die JS, Yu G, Jiang O
Dubell AN, Ratcliffe
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WPI; 2004-225755/21

LJ, Broun Samaha RS;

Kumimoto

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                                                                                                                                                                                                                                                          Constitutive, inducible or tissue-specific promoter and a recombinant constitutive, inducible or tissue-specific promoter and a recombinant colynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait; identifying a factor that is modilated by or interacts with a polypeptide encoded by the polynucleotide sequence that is subject to a regulatory effect of any of trait e.g. an enhanced tolerance to abject to a regulatory effect of any of trait e.g. an enhanced tolerance to abject to a sequence to failting, germination in cold conditions, freezing tolerance, tolerance to chilling, germination in cold conditions, freezing tolerance to fany of the polypuchten coldenance to sensitivity to mitrogen limitation, decreased sensitivity to introgen limitation), altered to be sensitivity to abtest acid, an altered the sensitivity to abtest acid, an altered susceptibility to producing a plant that has an altered conditions, freezing tolerance to deprive the sensitivity to abtest sensing, altered susceptibility to producing a plant that the sensitivity to abtest acid, an altered susceptibility to produce to express to ethylene, disease resistance, altered susceptibility to germination and seedling vigor, early flowering, latered susceptibility to germination and seedling vigor, early flowering, latered susceptibility to germination and seedling vigor, early flowering, latered manage, altered colder period of flowering, altered susceptibility to germination, altered susceptibility to provide seed derived trichome density, ectopic trichome development, altered seed development, altered branching pattern, reduced apical dominance, reduced trichome density, ectopic trichome development, altered seed state altered seed shape, change in leaf cell success in 
                                                                                                                                                                                       Matches
                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a transgenic plant comprises a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as AD001588-AD003527 or AD003530-AD003559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a
                                                                                                                                                                                                                                                        Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic plant, useful in developing phenotypes with altered improved characteristics or traits.
123 TCCATGGACGCCGGAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGG
                                                    102 ACAAGCCAATCCAATAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGGCTGAAGAAGGG
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                                                                           GGAAGGAGCAAGCAATGGGGAGGGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGG
                                                                                                                    GCTCCCTCCCGTCCCCAAAGACA-AACAGGCGAGCAGCAAACACACACGCTCGAACCGAG
                                                                                                                                                    GCCGCCTCCCTTCCAAGAACACACAACGCAAGAGGAGCAGAGCAGTTCAGATCAGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1058; 213pp; English.
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                                                                                                                                                                                    Score 366; DB 12;
Pred. No. 9.1e-63;
0; Mismatches 270;
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                                                                                                                                                                                                                                                       200 T; 0 U; 0 Other;
                                                                                                                                                                                                                     Length 1344;
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	243 282	CCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAGGA 302	ມ ນ
	303 342	GGACACCATCATCCATCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCGCCAG 362	F 53
	363 402	GTTGCCCGGGAGGACGACAACGAGATCAAGAACGTGTGGCACACCCACC	1 2
	423 462	CCTCGATGCGCCGGCTCAGGGCGGTCATGTCGCGGCGAGCGG 464	164
	465 522	CGGCAAGAAGCACAAGAAGCCGAAAGAAGCGC	۳ŏ
	501 582	GCCAGCCGCCGCCGCCGCCGCCGCCGCGCGCCCCAGCCGCC	P 0
	561 642	GACGGAGTCCTCGATGGCCTCGTCGGTGGCGGAGGAGCACGGCAACGCCGGGATCAGCTC 620	ρõ
	621 702	GGCGTCCGCGTGTGCGCCAAGGAGGAGAGCTCCTTCACCTCGGCTTCCGA 674	4
	675 762	GGAGTTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTGGA 728	μ <u>α</u>
	729 822	CGGGTACGACGTGTCCATGGAGCCCGGCGACG760	ř ö
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	810 942	GTTCATGGAGTCCGGCGAAGCGCAAGACTTGCCGCAGATCTAGAGAAAAGAGAGAGAA 866	<u> </u>
	867 1002	THTACCGTTTCTTCGGTTAAT-TGATTTGTTTTTTTCTCTCTCTGCGGCATCTTGCACC 925	<u> </u>
	926 1062	GGAGGGACATAGCTAACAGACAAGAGTGTCCATGAGCGAATCATCAAGCAGGAA 979	

ADX50163 standard; cDNA; 1126 BP

21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 24903.

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                                                                                                                                                                                                                 The invention describes a recombinant DNA construct comprising a CC polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide and as CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide construct is useful for CC improving plant tolerance to cold, heat, drought, herbicides, extreme CC consortic conditions, pathogens or pests, for manipulating growth rate in CC light cells by modification of the cell cycle pathway, for conferring CC light or plant growth regulators, for increasing the rate of homologous crecombination in plants, for improving yield by modification of CC content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert content.
                                                                                                                                   Query Match
Best Local S
Matches 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                    Sequence 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
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ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.
                                                                                                                                                Similarity
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CTGCCCAAGCAAGCCGGCTGCTGCGGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAAC
                                                    GAGGAGGACAAGGTCCTCGTCGCCCACATCCAGGGCCACGGCCACGGCAACTGGCGCCC
                                                                                      ATAATGGGGAGGGCTCCGTGCTGCGAGAAGATGGGGCCTGAAGAAGGGGGCCATGGACGCCC
                                                                                                  ACAATGGGGAGGGCTCCGTGCTGCCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 24903; 15pp; English
                                       GAGGAGGACAAGGTCCTGGTCGCCCACATCCAGAGCTTCGGCCACAGCAACTGGCGCGCG
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or for
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                                                                                        DNA;
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AGCCTCCACGAGCAGCTCGGCAACAGGTGGTCGGCCATCGCCGCCAGGCTGCCCGGGGGGG
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                                                                                                The invention describes a transgenic plant comprising a recombinant CC polynuclectide of any one of more than 500 nucleotide sequences fully CC defined in the specification or its complement. The method of the CC invention can be used to produced a plant having altered traits such as: CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone ce sensitivity; disease resistance; sugar sensing; early or late flowering; CC altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance; reduced trichome density; lack of CC trichomes; reduced ectopic trichome number; altered stem morphology; concreased root growth; increased not hairs; altered seed development; increased not contains; altered seed development; contains increased necrosis; increase in seedling or plant contains plant size; leaf morphology; seed morphology; seed biochemistry; increased not anthocyanins; increase in plant contains plant plant polynucleotides and polypeptides are useful in contains contains plant, polynucleotides and polypeptides are useful in contains contains search methods. This sequence represents a plant can search methods. This sequence represents a plant can search methods. This sequence represents a plant contains of a transgenic plant with altered traits.
Query Match
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Pilgrim ML,
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HAAKE V.
HAAKE V.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
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Dubell AN, Pineda O,
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                                                                                     TGCATCGGAGGGACGGACAAGGACAGCAGCAGCTGATTAACAGAGAAGGAAATCAGGCA
                                                                                                                                          TGCACCGGAGGGACATAGCTAACAGACAAGAGTGTCCATGAGCGAATCATCAAGCAGGAA
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                                                                                                                                                                                                                                                                                                                                                                GTGTTCATGGAGTCCGGCGAAGCGCA---AGACTTGCCGCAGATCTAGAGAAAAGAGAGAG
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0; Mismatches 224;
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AAGCCA

477 478 431 418 375 358 298 255 238

538

658 555 865 504

1138 979

1018

864 958 807 898 838

728

760

778

669 718 615

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Search completed: June 24, 2006, 19:33:39 Job time : 1462 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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 GenEmbl:*

1: gb_env:

2: gb_pat:

3: gb_pt:

5: gb_pr:

6: gb_rr:

7: gb_g
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1202
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Y11414 O. sativa mR
AY323484 Oryza sat
Continuation (259
AL731616 Oryza sat
AK111798 Oryza sat
AX659818 Sequence
AX653407 Sequence
AX6633407 Sequence
AX663347 Sequence
AX663364 Sequence
AX66354 Sequence
AX66373 Oryza sat
AX615199 Triticum
X99973 H. vulgare m
AK112056 Oryza sat
AX653760 Sequence
AY178579 Lolium pe
Y11350 O. sativa mR
AK1006021 Oryza sat
AX652852 Sequence
AK108621 Oryza sat
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Arbitoto Lea maye	NC967670	۵.	1389	18.1	217.8	<b>σ</b>
7,000 705 81	AF521880	4.	1038	18.2	$\boldsymbol{r}$	4
AJ311052 Oryza sat	OSA311052	4.	1429	18.3		w
11053 Oryza s	OSA311053	4.	1380	18.3	220.4	N
ea m	MZEPPR		1802	18.4	٠	
AF427146 Zea mays	AF427146		1513	18.4		0
BT008981 Triticum	BT008981		1199	18.4	•	9
CS137814 Sequence	CS137814		936	18.5	•	œ
U57002 Zea mays P	ZMU57002	4	1601	18.5	222.4	7
AK121023 Oryza sa	AK121023		4669	18.6	•	σ
AK111740 Oryza sat	AK111740		1450	18.6	•	v
AK106039 Oryza sa	AK106039		1139	18.6		4.
	D88618		1069	18.8	•	ω
CS137822 Sequence	CS137822		1369	18.8	•	N
AK063027 Oryza sa	AK063027		1027	18.9	•	_
CS138020 Sequence	CS138020		1027	18.9		0
BT009312 Triticum	BT009312		1336	19.0	228.2	9
CS137758 Sequence	CS137758		1026	19.3	231.4	8
	AY323480		1223	19.4	233	7
AX653762 Sequence	AX653762	N	1107	19.5		σ
	OSMYB1355	4	1355	19.5	234.8	5
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	AK111720	Δ.	1665	20.3	٠	ω
	AK111933	4.	1528	20.4	٠	N
e	AX652823	N	1023	20.4	245.8	_
Oryza	4	4.	1163	20.6	•	0
AK111960 Oryza sat	AK111960	4.	1637	20.7	249	φ

## ALIGNMENTS

	CDS	gene	source	FEATURES	AUTHORS TITLE JOURNAL	PUBMED	TITLE JOURNAL	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 OSMYB1202 LOCUS DEFINITION
/Godon start=1 /codon start=1 /protein id="CAA72217.1" /protein id="CAA72217.1" /db_xref="GI:1946265" /db_xref="GOA:004140" /db_xref="UniProtKB/TrEMBL:004140" /db_xref="UniProtKB/TrEMBL:004140"	/9:e="  \vec{y} u	/organish= Oryza sariva (Japonica curtival group) /mol type="manh" /culTivar="Arborio" /db xref="taxon:39947" /clone="OsMyB4" /tissue type="coleoptiles" /tissue type="coleoptiles" /dev_stage="three days old" 1. 1202 /capa-"mib"	11202	Location/Qualifiers	Coraggio,I.  Direct Submission Submitted (21-FEB-1997) I. Coraggio, Istituto Biosintesi Vegetali, CNR. Via Bassini 15., 20133. Milano, ITALY	9235602 2 (bases 1 to 1202)	1997)	<pre>Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza. 1 Pandolfi.D., Solinas.G., Valle.G. and Coraccio.I.</pre>	Y11414.1 GI:1946264  Y11414.1 GI:1946264  myb gene.  Oryza sativa (japonica cultivar-group)  Oryza sativa (japonica cultivar-group)  Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OSMYB1202 1202 bp mRNA linear PLN 18-APR-2005

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TCTCTCTCTGCCGCCATCTTGCACCGGAGGGACATAGCTAACAGACAAGAGTGTCCATGA
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                                         CCGCAGATCTAGAGÁAAGAGAGAGAATTTTACCGTTTCTTCGGTTAATTGATTTGTTTTT
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ilarity 100.0%;
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Pred. No. 3.7e-290;
; Mismatches 0;
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021-201106, China
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.
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Quanhong, Y., Rihe, P.
Direct Submission
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Quanhong, Y., Rihe, P.
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Feng, Q.,
Liu, Y., F
                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                          Oryza sativa genomic DNA, complete sequence.
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AL731616.5 GI:57834148
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Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, J.P., Fu, G., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, C.Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H. and Hong, G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan (http://ccr.081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/ENNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
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Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan,
Wu, M., Zhang, R., Zhou, B., Chen, Z., Chen, L., Jin, Z., Wang, R.,
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Li, J., Hong, G., Xue, Y. and Han, B.
Sequence and analysis of rice chromosome 4
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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VERSION
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AK111798
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                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                   Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., tohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, T., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Mateubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
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AKII1798.1 GI:37988461

FLI_CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hangaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Ilda,J., Ilda,Y., Ikeda,R., Imamura,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAACTGGATCATCAGAAAACGGGCTCTGCGTTTCTCATTTGATTAAATTTAAATTCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTATGTATAGAAACAGAAGAGATCAGTGATCGAAACCTGAGATCCTTTCTCACAATGTG
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                                                                                                                                                                                             lence 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice Full-Length cDNA Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1836 bp mRNA linear PLN 29-OCT-2003 cultivar-group) cDNA clone:J023105H16, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1178
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밁 8

Matches

846;

0

Mismatches

0

Gaps

1050

6.7e-201;

CAGGTGGTCCGCAATTGCCGCCAGGTTGCCCGGGAGGACGACAACGAGATCAAGAACGT 398

Local Similarity

FEATURES

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                           FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Foljimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Mikura,J., Oka,M., Xie,Q., Yokomizo,S., Yoshimura,A., Marikawa,R., Jisunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Adachi,J., Aizawa,K., Akhimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Sakayawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
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                                                                                                                                               /cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023105H16"
                                                                                                                                                                                                                                                       organism="Oryza sativa/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
70.4%;
100.0%;
Score 846;
Pred. No.
                                                                                                                                                                                                                                                                                                  (japonica cultivar-group)"
                                  DB 4;
                                  Length 1836;
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COMMENT

JOURNAL

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AX659818
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                  REFERENCE
AUTHORS
 TITLE
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                                                                                                 AX659818
Sequence 175
AX659818
AX659818.1 G
                                     Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Ehrhartoideae; Oryzeae; Oryza.
Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Plant disease resistance genes
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Syngenta Participations AG (CH)
Location/Qualifiers
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nilarity 98.4%;
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/mol_type="unassigned DNA"
/db_xref="taxon:4530"
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Pred. No. 1.8e-177;
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Oryza sativa
Cryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.
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                CGTGTCCATGGAGCCCGGCGACGCGTTCGTCGCGCCGCCATCCGCCGACGACGACATGGACTA
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Pred. No. 1.8e-175;
0; Mismatches 4;
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Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Ehrhartoideae; Oryzeae; Oryza.
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CTCGGCGTCCGTGTGCGCCAAGGAGGAGGAGCTCCTTCACCTCGGCTTCCGAGGA
                                                GGTGACGGAGTCCTCGATGGCCTCGGTCGGTGGCGAGGAGCACGGCAACGCCCGGGATCAG
                                                                                              TCAGGGCGGTCATGTCGCGGCGGCGGCGCAAGAAGCACAAGAAGCCGAAGAGCGCGAA
                                                                                                                                           GACAACGAGATCAAGAACGTGTGGCAC-ACCCACCTCAAGAAGCGCCTCGATGCGCCGGC
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/mol_type="unassigned DN
/db_xref="taxon:4530"
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Pred. No. 1.8e-175;
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a; Poales; Poaceae; BEP
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Matches 623; Conserv
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                      GCAACTGGCGCGCCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGC
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                                                                                                               GTCCATGGACGCCGGAGGAGAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACG
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                  TCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCAAGGAGGAGG
                                                      GCAACTGGCGCCCCCCCAAGCAAGCCAGGCTGCTGCGTTGCGGCAAGAGCTGCCGGC
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/product="myb protein"
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/protein_id="AAL78372.1"
/db_xref="GI:18698672"
/db_xref="GI:18698672"
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EIKNVWHTHLKKRLDAPAQGGHVAASGGKKHKKPKTRRSQPPPPPGRGVAERSARRR"
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Beidi Road 2901, Shanghai 201106, China
Location/Qualifiers
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/mol_type="mRNA"
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Accession Number AY034052"
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Pred. No. 8.9e-126;
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Chen,R., Ni,Z. and Sun,Q.
Direct Submission
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Chen, R., Ni, Z. and Sun, Q.
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          1044 bp aestivum transcription
                                                                                                                                                                                                                  /cultivar="3338"
/db_xref="taxon:4565"
/tissue_type="seed"
1. .1044
                                                                                                                                                                                    note="Tamyb2"
                                                                                                                                                                                                 'gene="Myb2"
                                                                                                                                                                                                                                                                                         organism="Triticum"
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                                                                                                                                                                                                                                                                           type="mRNA"
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Mingyuan Road, Haidian
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                          CATCAAGCAGGAAGAACGCGAATCATGC 994
                                                                                                                   CATCTTGCACCGGAGGGACATAGCTAACAGACAAGAGTGTCCATGAGCG------
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TAGTAGCCAGCAAGAACGCGGATCATGC 1043
                                                                                         CTTGCTGCACCGGAGGG--ATTGCTAACAGAGAGAGTGCGCTGCACCGTGGAGGAAAAT
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0; Mismatches 192;
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gubler, F., Roberts, J.K. and Jacobsen, J. Cloning of a cDNA Encoding a Novel Myb Expressed Layers (Accession No. X99973) (PGR97-013)
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Cloning of a CDNA Encoding a Nobel Myb
Layers (Accession X99973) (PGR97-013)
Plant Physiol. 113, 306-306 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-AUG-1996) F. Gubler, Co-operative Plant Science, PO Box 475, Canberra City, ACT, A
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                                                                                                                                                                                       CGGAGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACCGGCAACTGGCGCG
                                                                                         CCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCCTGCCGGCTCCGGTGGATCA
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/gene="myb4"
/codon_start=3
/product="myb4 transcription factor"
/db_xref="G1:1617325"
/db_xref="G1:1617325"
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/db_xref="taxon:112509"
/clone="H112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare
/mol_type="mRNA"
/cultivar="Himalaya"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="aleurone layer"
/tissue_type="endosperm"
/clone_lib="lambda ZAP II"
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                  The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Octomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Mazuno, K., Yokomizo, S., Niikura, J., Kurosaki, T., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ireda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
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FII CDNA; oligo capping.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Spermatophyta; Magnoliophyta; Clade; Ehrhartoideae; Oryzaee; Oryza.
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Oryza sativa (japonica cultivar-group) cDNA clone:001-110-C03, full
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AK112056.1 GI:37988719
Collection, mapping, and annotation of over 28,000 cDNA clones from
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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., RS Adachi, J., Fukuda, S., Hanagaki, T., Hara, A., Hashirume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashirume, W., Fujimura, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotte, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakahama, Y., Namizano, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Namizano, K., Nunasaki, R., Ohneda, E., Ohno, M., Ohsuki, K., Oka, M., Ooka, H., Osaco, N., Ota, Y., Otmoy, Y., Ryu, R., Saitoh, K., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shihata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Shiraki, T., Suzuki, Y., Tagami, M., Tanaka, T., Tasanda, T., Tasanda, T., Takaku-Akahira, S., Yacomiyo, S., and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomiyo, S., and Yoshimura, A.
                                                                                                                                                                                                                                                                            PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Ifiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurih, H., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami, M., Sano, H., Sasaki, D., Sato, K., Shibata, K., Yasunishi, A., and Hayashizaki, Y. Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
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Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007)
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Ehrhartoldeae; Oryzeae; Oryza.
           Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. & Plant genes involved in defense against pathogens Patent: WO 0300089-A 3630 03-JAN-2003; Syngenta Participations AG (CH) Location/Qualifiers
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Lolium perenne F
AY178579
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnollophyta; Liliopsida;
clade; Pooideae; Poeae; Lolium.
1 (bases 1 to 330)
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                                                                                                                         Unpublished

2 (harmal ryegrass
                                                  Larsen, K.
Direct Submission
Submitted (13-NOV-2002) Department
Science, Danish Institute of Agricu
Tjele DK-8830, Denmark
                                                                                                                                                              Cloning of MYB transcription
                                                                                                                                                                                                                                                          Lolium
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/mol_type="unassigned DN
/db_xref="taxon:4530"
/organism="Lolium
/mol_type="mRNA"
                                       Location/Qualifiers
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Pred. No. 4.9e-
1; Mismatches
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myb gene.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1084)
Solinas G., Valle,G., Pandolfi,D. and Coraggio,I.
The electronic Plant Gene Register
Plant Physiol. 114 (2), 747-749 (1997)
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                                                                                                                          Direct Submission
Submitted (18-FEB-1997) I. Coraggio, CNR, Istituto
Submitted (18-FEB-1997) I. Coraggio, CNR, Istituto
Vegetali, Via Bassini 15, Milano, 20131, ITALY
Location/Qualifiers
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O.sativa mRNA for myb
Y11350
Y11350.1 GI:1945278
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/note="LpMYB4; WYB transcription factor"
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1...>330
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Pred. No. 2e-56;
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"SEFWSSTEVTGMMAGLGDMDEELAIAGTSSAAAARRSDDMEFWLKMLLESGDMRDLAVL
"SFWSSTEVTGMMAGLGDMDEELAIAGTSSAAAARRSDDMEFWLKMLLESGDMRDLAVL"
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/dev_stage="three days old
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1: geneseqp198
2: geneseqp199
3: geneseqp200
4: geneseqp200
6: geneseqp200
6: geneseqp200
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1368
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Maximum Match 10
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            geneseqp2004s:*
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Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	υı	4	ω	2	1	200	Result
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46.8	46.8	46.8	46.8	46.8	46.8	46.8	46.9	48.1	48.4	48.4	48.4	48.9	50.0	54.6	55.7	55.7	58.4	58.4	60.5	60.5	84.3	84.3	Match	
273	273	273	273	273	273	273	260	313	304	285	.285	278	277	248	162	162	309	257	258	258	257	257	тепдсп	
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The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a prote

conferring disease resistance used

present sequence represents in the invention.

resistance or esents a prote

protein

New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant

Claim 10; SEQ ID NO 722; 299pp; English.

pathogen.

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563	582	582	584	592	593	597	601	109	601	606.5	608	623.5	626.5	626.5	628.5	640	640	640	640	640	040
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Adw18468	Add55856	Abo43148	Adw17784	Adw17378	Adx94416	Aag26239	Ado02409	Ada15467	Aae02557	Aag41252	Aag30515	Ado01703	Adh50134	Abj10425	Aec91871	Adz67575	Ado01743	Ado01751	Ado03341	Adi43515	VICTRIDA
Pinus rad	Thalecres	A. thalia	Pinus rad	Eucalyptu	Plant ful	Arabidops	Thalecres	A. thalia	₽	Ara			Rice Myb-	Myb-relat	Thale cre	Arabidops	Thalecres	Thalecres	Thalecres	Plant tra	בזמוור רומ

## ALIGNMENTS

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RESULT 1
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WPI; 2003-184052/18.
N-PSDB; ADA48651.
                                                                                                                                    Glazebrook J, Brig
Katagiri F, Kreps
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                       21-JUN-2002; 2002WO-IB002453.
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                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                  disease resistance;
                                                                                                                                                                                                                                                                                Rice protein conferring disease resistance in plants
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                                                                                                                                                                                                                                                                                                                             ADA48652 standard; protein;
                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                    Briggs S, Cooper B, Goff SA,
reps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                  pathogen tolerance; plant pathogen; plant; rice.
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                                                                                                                                     Zhu
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Best Local S
Matches 222
                     The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test
                                                                                                                                                                                                                                                                                 New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress
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                                                                                                                                                                                                       Claim 1;
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24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
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222; Conser
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                                                                                                                                                                                                     SEQ ID NO 8888; 89pp; English.
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T, Provart
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  exposed to an abiotic
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84.1%; Pred. No. 6.4e-103;
tive 11; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                          Cooper B,
N, Ricke
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D, Zhu T;
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     condition.
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Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homol ortholog to an abiotic stress responsive polynucleotide. The nucle molecule and the polypeptide encoded by it are useful in altering responsiveness of a plant to an abiotic stress, such as cold stress stress or any of their combinations. The present is used in the exemplification of the invention
  Claim
                                         Novel isolated polynucleotide useful for fragment encoding a Myb-related transcrip
                                                                                                                                                                           Cahoon RE,
                                                                                                                                                                                                                                                                                    (CAHO/)
                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1999;
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RAFALSKI J .
SHI J.
WENG Z.
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1; Mismatches 17;
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RESULT 4
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Best Local Sim:
Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated polynucleotide comprising a CC first nucleotide encoding a polypeptide of 217, 120, or 268 amino acids that has 85%, 95%, or 96% identity based on the clustal method of CC that has 85%, 95%, or 96% identity based on the clustal method of CC alignment when compared to a polypeptide selected from Myb polypeptides gequences of 128, 258, or 268 amino acids fully defined in the CC specification, or a second nucleotide sequence comprising the complement of the first nucleotide. The isolated polynucleotide is useful for Obtaining a nucleic acid fragment encoding an Myb-related transcription factor polypeptide by using it to probe CDNA or genomic libraries. A nucleic acid fragment obtained using the isolated polynucleotide is useful to isolate cDNAs and genes encoding homologous proteins from the cuseful to isolate cDNAs and genes encoding homologous proteins from the same or other plants in which the Myb-like protein is present at higher or lower levels than normal or in cell types. This sequence represents the protein of an Myb-related transcription factor of the
                                                                                                                                                                                                                                                                                                                                                                                               ADH50100 standard;
Cahoon RE,
                                                                                                                                                                                       US2002187539-A1
                                                                                                                                                                                                                     Oryza sativa
                                                                                                                                                                                                                                                                   Myb-related transcription
                                                                                                                                                                                                                                                                                                                                  25-MAR-2004
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                                                                                                                                                         12-DEC
                                                                           20-NOV-1998;
19-NOV-1999;
                                                                                                                        05-DEC-2001; 2001US-00008118
                             (CAHO/) CAHOON R E. (WENG/) WENG Z.
                                                                                                                                                                                                                                                                                                  Myb-related transcription factor #1.
                                                                                                                                                                                                                                                  regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSMASSADHUT----TDSFTS-EEEFQIDDSFWSETLAMTVDSTDSGMEMSGGDPLGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNAGISSASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSME-----PGDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGREAAA----PKRKATKKAAAVAVAIDVPTTVPVSPEQSLSTTTT----SAATTEEY
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Weng
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                                                                          98US-0109294P
99US-00443704
73
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                                                                                                                                                                                                                                                                     factor;
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Pred. No. 2.3e-71;
                                                                                                                                                                                                                                                                     transcriptional
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RESULT 5
AAG54569
ID AAG5
XX AAG5
XX AAG5
XX AAG5
XX Eea
XX Prot
KW Prot
KW hybr
KW tern
XX Zea
XX Zea
XX Een1
XX Een1
XX E91
PN 25-1
PR 25-1
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PR 23-1
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Best Local S
Matches 169
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of Mybrelated transcription factors - these proteins are involved in transcriptional regulation in plants. The DNA and protein sequences of the invention may be used to facilitate studies to better understand gene regulation in plants and provide genetic tools to enhance or otherwise alter the expression of genes controlled by Myb-related transcription factors. The present amino acid sequence represents an Myb-related transcription factor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new isolated plant transcription factor
                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway;
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N-PSDB; ADH50099.
                                                                              25-FEB-2000;
                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                     Zea mays protein fragment
                                                                                                                                                                                                                                                               18-OCT-2000
                                                                                                                                                                                                                                                                                          AAG54569;
                                                                                                                                                                                                                                                                                                                  AAG54569 standard;
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                                                                               2000EP-00301439
                                                                                                                                                                                                                                                              (first entry)
 99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
                                                                                                                                                          mays
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                                                                                                                                                                                   corn.
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Pred. No. 2.3e<sup>2</sup>
29; Mismatches
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No. 2.3e-71;
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19-UIL-1999; 99US-0144331 19-UIL-1999; 99US-0144331 19-UIL-1999; 99US-0144332 20-UIL-1999; 99US-0144332 20-UIL-1999; 99US-0144332 20-UIL-1999; 99US-0144632 20-UIL-1999; 99US-0145086 21-UIL-1999; 99US-0145086 21-UIL-1999; 99US-0145086 21-UIL-1999; 99US-0145145 23-UIL-1999; 99US-0146386 24-UIL-1999; 99US-0146386 27-UIL-1999; 99US-0147038 03-UIG-1999; 99US-0147038 03-UIG-1999; 99US-0147038 04-UIG-1999; 99US-0147038 05-UIG-1999; 99US-0147038 07-UIG-1999; 99US-0147038 07-UIG-1999; 99US-0147038 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0147036 07-UIG-1999; 99US-0151066 07-UIG-1999; 99US-	9US-0142803 9US-0142977 9US-0143542 9US-0143624 9US-0144065 9US-0144085	9US-0141287 9US-0141287 9US-0141842 9US-0142154 9US-0142055 9US-0142390	9US-0139817 9US-0139899 9US-0140353 9US-0140354 9US-0140695 9US-0140823 9US-0140991	9US-0139459 9US-0139469 9US-0139461 9US-0139462 9US-0139463 9US-0139750 9US-0139750	9US-0139119 9US-0139453 9US-0139453 9US-0139492 9US-0139454 9US-0139456 9US-0139456	903-013533 903-0135629 903-0136021 903-0136392 903-0136782 903-0137528 903-0137528 903-0137502 903-0138502 903-0138540	9US-0132485 9US-0132487 9US-0132863 9US-0134256 9US-0134218 9US-0134218 9US-0134219 9US-0134291 9US-0134291	9US-0127462 9US-012746234 9US-0128234 9US-0128714 9US-0130077 9US-0130140 9US-0130891 9US-0131449 9US-0132447 9US-0132407
19-JUL-1999; 99US-0144331 19-JUL-1999; 99US-0144331 19-JUL-1999; 99US-0144332 20-JUL-1999; 99US-0144332 20-JUL-1999; 99US-0144632 20-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 22-JUL-1999; 99US-0145086 22-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0145086 24-JUL-1999; 99US-0145086 27-JUL-1999; 99US-0146388 02-AUG-1999; 99US-0146388 02-AUG-1999; 99US-0147038 03-AUG-1999; 99US-0147038 04-AUG-1999; 99US-0147038 05-AUG-1999; 99US-0147038 07-AUG-1999; 99US-0147038 07-AUG-1999; 99US-0147038 07-AUG-1999; 99US-0147038 07-AUG-1999; 99US-0147036 07-AUG-1999; 99US-0147036 07-AUG-1999; 99US-0147038 07-AUG-1999; 99US-0147036 07-AUG-1999; 99US-0150666 07-AUG-1999; 99US-								
19-JUL-1999; 99US-0144331 19-JUL-1999; 99US-0144331 19-JUL-1999; 99US-0144332 20-JUL-1999; 99US-0144352 20-JUL-1999; 99US-0144834 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 21-JUL-1999; 99US-0145086 22-JUL-1999; 99US-0145086 22-JUL-1999; 99US-0145086 23-JUL-1999; 99US-0146388 02-AUG-1999; 99US-0146388 02-AUG-1999; 99US-0147038 03-AUG-1999; 99US-0147036 03-AUG-1999; 99US-0151066 03-AUG-1999; 99US-								
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RESULT 6
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AC AAG5
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DT 18-C
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18-OCT-1999
21-OCT-1999
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21-OCT-1999
22-OCT-1999
                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                    AAG54568;
             EP1033405-A2
                                                                                                                           18-OCT
                                                                                                                                                                           AAG54568 standard;
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                                   mays subsp.
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99US-0159294p

99US-0159295p

99US-0159330p

99US-0159331p

99US-0159331p

99US-0159638p

99US-0160741p

99US-0160741p

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99US-0160814p

99US-0160814p

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99US-0161404p

99US-0161350p

99US-0161350p

99US-0161361p

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  25-FEB-1999
05-MAR-1999
09-MAR-1999
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21-APR-1999
01-APR-1999
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 99US-0121825P
99US-0123548P
99US-0125788P
99US-0126764P
99US-0126764P
99US-0126785P
99US-0126785P
99US-01300479P
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99US-0132048P
99US-0132484P
99US-0132484P
99US-013421P
99US-013945P
99US-0140695P
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99US-0141287P
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06-JUL-1999 08-JUL-1999 09-JUL-1999 12-JUL-1999 13-JUL-1999 14-JUL-1999 15-JUL-1999

6-JUL-1999; 8-JUL-1999; 9-JUL-1999; 2-JUL-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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RESULT 7
ADA48106
ID ADA4
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AC ADA4
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DT 20-N
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Rice
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Best Local S
Matches 160
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Rice protein conferring disease resistance in
                          ADA48106;
                                     ADA48106
            20-NOV-2003
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                                                                                                                                                                                                       Similarity
                                                                                                                                              HGNAGISSASASVCAKEESSFTSASEEFQIDDSFWSETLSM--PLDGYDVSMEPGDA---
                                      standard;
                                                                                                                     AQGGHVAASGGKKHKKPKSAKKPAAAAAAP----PASPERSAS--SSVTESSMASSVAEE
                                                                    KSAAPPSSTNDDMDFWLKLFMQASDMQNLPQI 308
                                                                            -FVAPPSA--DDMDYWLGVFMESGEAQDLPQI
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            (first entry)
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-0169294p.
-016074p.
-016076p.
-0161360p.
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                                      162
                                                                                                                                                                                                Score 799.5; DB 3;
Pred. No. 1.5e-68;
0; Mismatches 51;
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plants
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                                                                                                                                                                                                             Length
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99US - 0142390P 99US - 0142920P 99US - 0142977P 99US - 014325P 99US - 0144325P 99US - 0144333P 99US - 0144334P 99US - 0145089P 99US - 0145089P 99US - 0145089P 99US - 0145192P 99US - 0145192P 99US - 0145218P 99US - 0145218P 99US - 0147303P 99US - 0147303P 99US - 0147303P 99US - 0147303P 99US - 014973P 99US - 0151303P 99US - 0151303P 99US - 015333P 99US - 015375P 99US - 0154018P 99US - 0154779P 99US - 0154779P

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Best Local Simi
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glazebrook .
Katagiri F,
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
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             WO2003008540-A2
                                                                                     Rice abiotic stress responsive
                                                                                                             02-JUN-2005
                                                                                                                                      ABM85964;
                                                                                                                                                              ABM85964 standard;
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DB; ADA48105.
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                                                                                                                                                                                                                                                                                                                                            MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQ-AGLLRCGKSCRLRWIN
                                                                                                                                                                                                                                                 PAQGGHVAASGGKKHKKPKSAKKPAAAAAA---PPASPER
                                                                                                                                                                                                                                                                                                                             MGKAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAAGLLRCGKSCRLRWIN
                                                                                                                                                                                                                                                                             YLRPDIKRGNFSKEEEDTIIHLHELLGNSRWSAIAARFPGRTDNGIKNVWTTHLKKRLDA
                                                                                                                                                                                                                             PÄQGGHVAASGGKKHKKPKSAKKPÄAADAGRRRRPSGPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 176; 299pp; English.
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                                                            tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                              protein;
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                                                                                                             entry)
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Pred. No. 2.3e-65;
2; Mismatches 8;
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                                                                                   polypeptide SEQ ID
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18-OCT-2000

(first entry

Zea mays protein fragment SEQ

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69593.

pathway; metabolic

pathway;
promoter;

AAG54570

standard;

protein;

248

118 120

60 59

Protein identification; signal transduction pathway; r hybridisation assay; genetic mapping; gene expression

sequence;

EP1033405-A2

Zea mays subsp. termination

mays

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RESULT 9
AAG54570
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                                                                                                                                                                                                                                                                                                         CC and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are CC methods for using the polynucleotides and polypeptides to alter the CC responsiveness of a plant to abiotic stress. The invention is useful in CC agriculture. The nucleic acid is useful for determining whether a test CC plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated CC polynucleotide expression in a plant cell, and to identify a homolog or cortholog to an abiotic stress responsive polynucleotide. The nucleic acid CC molecule and the polypeptide encoded by it are useful in altering the CC responsiveness of a plant to oan abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
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Best Local S
Matches 145
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Moughamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                         Sequence 162
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26-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-248011/24.
                                                                                           119
                                                              121
                                                                                                                                                                                                                                               145;
                                                                                                                       13
                                                                                                                                                     60
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                    MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQ-AGLLRCGKSCRLRWIN
                                                                                                                                                                                   MGKAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAAGLLRCGKSCRLRWIN
                                                             PAQGGHVAASGGKKHKKPKSAKKPAAADAGRRRRPSGPPR
                                                                              PAQGGHVAASGGKKHKKPKSAKKPAAAAAA---PPASPER
                                                                                                                         YLRPDIKRGNFSKEEEDTIIHLHELLGNSRWSAIAARFPGRTDNGIKNVWTTHLKKRLDA
                                                                                                                                        YLRPDIKRGNFSKEEEDTIIHLHELLGN-RWSAIAARLPGRTDNEIKNVWHTHLKKRLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Briggs SP,
T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                             55.7%;
90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper B, G
N, Ricke D,
                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                               Score 762.5;
Pred. No. 2.3e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glazebrook
D, Zhu T;
                                                                                                                                                                                                                                                              .3e-65;
                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for altering the an abiotic stress
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                                                                                                                                                                                                                                                                           7;
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                                                                                            155
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                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such
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99US-013077P- 99US-013077P- 99US-0130449P- 99US-0131449P- 99US-0132407P- 99US-0132407P- 99US-0132486P- 99US-0132486P- 99US-0132486P- 99US-0134256P- 99US-0134218P- 99US-013421P- 99US-013421P- 99US-013421P- 99US-013421P- 99US-0135224P- 99US-0135224P- 99US-0135224P- 99US-013522P- 99US-0137222P- 99US-0137222P- 99US-0137222P- 99US-0137222P- 99US-013945P- 99US-013963P- 99US-013963P- 99US-0140053P- 99US-0141087P- 99US-0141087P- 99US-0141087P- 99US-0141087P- 99US-0141087P- 99US-0141087P- 99US-0141087P-	0EP-0030143 9US-0121825 9US-0123548 9US-0125788 9US-012678 9US-012678 9US-012678 9US-012678
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99US-0144335P 99US-014484P 99US-0144884P 99US-0145085P 99US-0145085P 99US-0145087P 99US-0145087P 99US-0145087P 99US-0145218P 99US-0145218P 99US-0145276P 99US-0145276P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0147302P 99US-0147302P 99US-0147303P 99US-0147303P 99US-0149175P 99US-0149175P 99US-0149175P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-0149368P 99US-015566P 99US-0151308P 99US-0151308P 99US-0151308P 99US-0151330P 99US-0151330P 99US-0154018P 99US-0154039P 99US-0154039P 99US-0154039P	9US-0142055 9US-0142390 9US-0142802 9US-0142977 9US-0143542 9US-0143524 9US-0144085 9US-0144085 9US-0144085 9US-0144233 9US-0144333

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RESULT 10
ADI42106
ID ADI42
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AC ADI42
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DT 22-AP
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Best Local Sim
Matches 152;
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14-007-1
14-007-1
18-007-1
21-007-1
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28-007-1
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08-OCT-1999;
         22-APR-2004
                           ADI42106;
                                              ADI42106 standard;
                                                                                                                                                                                                                                                                                                                                                    G-OCT-1999;
G-OCT-1999;
G-OCT-1999;
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                                                                                                                                174
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                                                                                                                                                                      118
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                                                                                                                                                                                                                                                                  10
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                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                         GGKKHKKPKSAKKPAAAAAAP----PASPERSAS--SSVTESSMASSVAEEHGNAGISSA
                                                                                                                                                                                                                    FSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD-APAQGGHVAAS
                                                                                                                                                                                                                                                         MGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINYLRPDIKRGN
                                                                                                                                                                     KRKPTKKQQPQPEPVTALEGPTGAVPVSPERSLSTTTSTTTSTADYSAASSLENAG----
                                                                                                                                                                                                           FSREEEDAIIQLHQMLGNRWSTIAARLPGRTDNEIKNVWHTHLKKRLEPKPAS----QQAP
                                                                                                                                                                                                                                               MGLKRGPWTAEEDRILVAHVERHGHSNWRALPKQAGLLRCGKSCRLRWINYLRPDIKRGN
                                                                                            NDDMDFWLKLFMQASDMQNLPQI
                                                                                                              -DDMDYWLGVFMESGEAQDLPQI 257
                                                                                                                               -----DSFTSEEDYYQIDDSFWSETLAMTTTVDSFESGVQQAEGSFGKSAAPPSST
                                                                                                                                                                                                                                                                                     Conservative
         (first entry)
                                                                                                                                                                                                                                                                                                                        99US-0155139P

99US-0155458P

99US-0156559P

99US-0155659P

99US-0157753P

99US-0157865P

99US-0159239P

99US-0159239P

99US-0159239P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0160767P

99US-0160768P

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99US-0160768P

99US-0160818P

99US-0160818P

99US-0160818P

99US-0160818P

99US-0160818P

99US-0161350P

99US-0161350P

99US-0161350P

99US-0161350P

99US-0161350P

99US-0161350P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P

99US-0161361P
                                             protein;
                                                                                                                                                                                                                                                                                            54.6%;
                                                                                                                                                                                                                                                                                    29;
                                              277
                                                                                                                                                                                                                                                                                             Score 747.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                     Mismatches
                                              ₿
                                                                                             247
                                                                                                                                                                                                                                                                                    5; DB 3;
1.2e-63;
hes 51;
                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                       248;
                                                                                                                                                                                                                                                                                    31,
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Gaps

182

235 173

Sequence 277

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transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; gene; ds.
                        pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered stem morphology; altered cell proliferation or cell differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabidopsis thaliana transcription factor; solated in the invention, that can be used in the creation of a transgenic plant with altered traits.
                                                                                                                                                                                                                                                                 The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherman BK,
Creelman RA,
                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transgenic plant comprising a recombinant polynucleotide of any o
of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-132245/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KEDD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ADAM/)
(REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2003; 2003US-00374780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001US-00837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004019927-A1
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RIECHANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
DUBELL A N.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PINEDA
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 569; 435pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riechmann JL, Jiang C, I
Ratcliffe O, Adam LJ, I
Dubell AN, Pineda O, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲
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Reuber
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Keddie ,
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RESULT 11
AAW37811
ID AAW37811
ID AAW377
XX AAW37
XX AAW37
XX 17-OC
DT 17-OC
DT 17-OC
DT 17-OC
DT 17-OC
DT 17-OC
T 17-OC
C TObac
XX TObac
XX TObac
XX WO981
XX WO981
XX WO981
XX AC
PT Regic
FT Tobac
FT Yang
XX Tobac
FT Tobac
FT With
XX Tobac
FT TO
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Best Local Similarity
Matches 144; Conserv
 This 32 kDa protein, designated Myb1, is the tobacco homologue of mammalian Myb and is involved in the regulation of disease resistance.
                                                                                    Tobacco mybl gene sequence - useful with improved disease resistance.
                                                   Claim 17; Fig 1A; 66pp; English
                                                                                                                                                           WPI; 1998-230699/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco Myb1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
17-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW37811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW37811 standard; protein; 278
                                                                                                                                                                                                                                                                  27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                        02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tobacco; Mybl protein; transgenic plant; disease resistance.
                                                                                                                                                                                                                                                                                                     26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                         WO9813486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                 (RUTF )
                                                                                                                                                                                             Y, Klessig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
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                                                                                                                                                                                                                                 UNIV RUTGERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSNTHDHVMVTADQELQVQLPFSSLKEENVDMLTTKMEDDMDFWYNVFIKTDDLPELPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TEMSTVTLV-DDH------QNVIKQEE--MESSEYFPEIDESFWTDKLSTDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVTESSMASSVAEEHGNAGISSASASVCAKEESSFTSASEEF-QIDDSFWSETLSMP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRPDIKRGNFTKEEBDTIIQLHEMLGNRWSAIAAKLPGRTDNBIKNVWHTHLKKKKLKDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LDGYDVSMEPGDA------FVAPPSADDMDYWLGVFMESGEAQDLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPO-----NPKRHSKNHDSKGPTTSESSNNSHLTFIYTOKHIIDSSVPAPNSPQISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAQGGHVAASGGKKHKKPKSAKKPAAAAAA-------PPASPERSAS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGRAPCCEKMGLKKGPWTPEEDQILISFIQQNGHGNWRALPKQAGLLRCGKSCRLRWTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tabacum; cv. Xanthi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                  96US-00722626
                                                                                                                                                                                                                                                                                                   97WO-US017415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "imperfect tryptophan repeat"
53
                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
179. .2
                                                                                                                                                                                             DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "conserved redox sensitive Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            . 278
                                                                                                                                                                                                                                 STATE
                                                                                                                                                                                                                                                                                                                                                                                                          "acidic C-terminal region"
                                                                                                                                                                                                                                                                                                                                                                                                                                           "imperfect tryptophan repeat"
                                                                                                                                                                                                                                 NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 684; DB 8;
; Pred. No. 2.1e-57;
37; Mismatches 52
                                                                                                                                                                                                                                 JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                      for,
                                                                                                      e.g. producing transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
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Best Local Similarity 47.2
Matches 141; Conservative
                                                   25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
   08-APR-1999;
16-APR-1999;
19-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 278 AA;
                                                                                                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                                                                                      EP1033405-A2
                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                         termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                   2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                     99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
                    99US-
                                                                                                                                             99US-0123180P.
99US-0123548P.
                                                                                                                                                                                99US-0121825P
                    S-0128714P.
S-0129845P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 AA
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Its amino acid sequence was deduced from an isolated cDNA clone (see AAV19105). The encoded protein comprises a basic N-terminal region with 2 imperfect tryptophan repeats, a potential ATP/GTP binding site or P-loop, a redox sensitive cysteine and a nuclear localisation sequence. The acidic C-terminus forms amphipathic alpha-helices which are characteristic of transcriptional activation domains. The Mybl protein can be used to identify other proteins involved in both the hypersensitive and acquired disease resistant responses of plants, and also to raise Mybl-specific antibodies. The invention also provides novel transgenic plants, transformed with a vector including the mybl gene, with enhanced disease resistance to certain pathogens. (Updated on 17-OCT -2003 to standardise OS field)
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LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD--A 118
                                                                                                                                                                                                                                                                                                                                                              MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
STDHVMVAANQELQVQLPFSSF---KEENVDILATKMEDDMDFWYNVFIKTDDLPELPE
                                                                                                                           VTESSMASSVAEEHGNAGISSASASVCAKEESSFTSASEEF-QIDDSFWSETLS-----
                                                                                                                                                                     PPQ-----NSKRHSKSKNHDSKGPTTSESSNNSDLTIINTQKHIDSPVLAPNSPQISS
                                                                                                                                                                                                        PAQGGHVAASGGKKHKKPKS--AKKPAAAAA------APPASPERSASSS
                                                                                                                                                                                                                                                                                                                                        MVRAPCCEKMGLKKGPWIPEEDQILISFIQTNGHGNWRALPKQAGLLRCGKSCRLRWTNY
                                         ----MPLDGYDVSMEPGDAFVAPPSADDMDYWLGVFMESGEAQDLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 669.5; DB 2; ; Pred. No. 5.2e-56; 37; Mismatches 56;
                                                                                   -QMVVIKQE--VMESSEYFPEIDESFWTDELTTDNNWS
                                                                                                                                                                                                                                                                                                                                                                                                                          56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278;
                                                                                                                                                                                                                                                                                                                                                                                                                            65;
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  277
                                            256
                                                                                                                                                                       173
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Protein identification; signal transduction hybridisation assay; genetic mapping; gene e Arabidopsis thaliana protein fragment SEQ ID NO: 51301. gene expression control;

pathway;
promoter;

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04-MAY-1999 05-MAY-1999 06-MAY-1999 11-MAY-1999 11-MAY-1999 11-MAY-1999 11-MAY-1999 11-MAY-1999 12-MAY-1999 12-MAY-1999 12-MAY-1999 13-MAY-1999 13-MAY-1999 13-MAY-1999 13-MAY-1999 13-JUN-1999 13-JUN	000000
99US-0132484P 99US-0132485P 99US-0132486P 99US-013425P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013421P 99US-013523P 99US-013523P 99US-013622P 99US-0137528P 99US-0137528P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-013943P 99US-014085P 99US-014085P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P 99US-014333P	08-013 08-013 08-013
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99US-0145089P 99US-0145089P 99US-0145089P 99US-0145192P 99US-01452145P 99US-01452149P 99US-0145218P 99US-0145918P 99US-0145918P 99US-0145918P 99US-0145918P 99US-0145918P 99US-0146388P 99US-0146388P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0147303P 99US-0149723P 99US-0149723P 99US-0149723P 99US-0151065P 99US-0151068P 99US-0151068P 99US-01513080P 99US-01513080P 99US-01513080P 99US-01513080P 99US-01513889P 99US-0158369P 99US-0159329P 99US-0159329P	US-0144352 US-0144632 US-0144884 US-0144814 US-0145086

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RESULT 13
ADN72611
ID ADN72
XX ADN72
AC ADN72
AC ADN72
XX 15-JU
XX 15-JU
XX Plant
KW Plant
KW anima
KW anima
KW anima
XX No200
XX 29-AP
PF 20-OC
XX 18-OC
XX 18-OC
XX
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Best Local Sim
Matches 146;
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14-0CT-1999
14-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
22-0CT-1999
22-0CT-1999
22-0CT-1999
22-0CT-1999
           18-OCT-2002; 2002EP-00079408
                                                                                                 Arabidopsis thaliana
                                                                                                                     plant; transgenic; E2Fa/DPa transcription factor; growth animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                20-OCT-2003; 2003WO-EP011658
                                                                            WO2004035798-A2
                                                                                                                                                                  Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID
                                                                                                                                                                                         15-JUL-2004
                                                                                                                                                                                                                                     ADN72611 standard; protein; 285
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                                                                                                                                                                                                                                                                                                                                        164
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                                                                                                                                                                                                                                                                                                                  LSMPLDGYDVS-----MEPGDAFVAPPSAD-----DMDYWLGVFMESGEAQDL 254
                                                                                                                                                                                                                                                                                                                                       LFSTSPSTSEVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKET
                                                                                                                                                                                                                                                                                                                                                              SASASVCAKEESSFTSASEE-------
                                                                                                                                                                                                                                                                                                                                                                                  QPAKPKTSNKKKGTKPKS------ESVITSSNSTRSESELÅDS----SNPSGES
                                                                                                                                                                                                                                                                                                                                                                                               QGGHVAASGGKKHKKPKSAKKPAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                                                                                                                                                                                                                                                                                               LKPDIKRGNFTKEEEDAIISLHQILGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLE-DY
                                                                                                                                                                                                                                                                                                                                                                                                                                          LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKKLDAPA
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                                                                                                                                                                                                                                                                                          LYSQDEHNYVSNDLEVAGLVEIQQEFQNLGSANNEMIFDSEMDFWFDVLARTGGEQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGRAPCCEKMGLKRGPWTPEEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNY
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                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159331p
99US-0159638p
99US-0160741p
99US-0160768p
99US-0160768p
99US-0160815p
99US-0160815p
99US-0160815p
99US-0161404p
99US-0161406p
99US-0161361p
99US-0161361p
99US-0161361p
99US-0161361p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.4%; Sc
49.0%; Pr
tive 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 661.5;
Pred. No. 3.2
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                                                                                                                                              growth regulator
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                                                                                                                                                                                                                                                                                                                                                              -----FQIDDSFWSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                              211
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RESULT 14 ADX91441

ADX91441

standard;

protein;

XXXXXXXXXX

21-APR-2005

(first entry

plant protectant; plant growth regulant; gene therapy; plant;

Plant full length insert polypeptide segid 54105

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CE 2Fa/Dpa transcription factor of Arabidopsis and using these sequences to CC alter plant characteristics accordingly. The present invention describes CC generating transgenic plants for the production of growth regulators, where CC enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or physiology, altered endoreduplication, blochemistry, signal CC transduction, storage lipid mobilisation and/or altered photosynthesis, CC each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers CC role in a variety of biological processes such as DNA replication, cell coli in a variety of biological processes such as DNA replication, cell constraint factors. This polypeptide sequence is thale cress protein convertion.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more proteins.
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                      LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                                                     MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                       LFSTSPSTSEVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKET
                                                                                                           SASASVCAKEESSFTSASEE----
                                                                                                                                                                                                                     LKPDIKRGNFTKEEEDAIISLHQILGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLE-DY
                                                                                                                                                                                                                                                                                            MGRAPCCEKMGLKRGPWTPEEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 506; 134pp; English
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LYSQDEHNYVSNDLEVAGLVEIQQEFQNLGSANNEMIFDSEMDFWFDVLARTGGEQDL
                                    LSMPLDGYDVS-----MEPGDAFVAPPSAD-----DMDYWLGVFMESGEAQDL 254
                                                                                                                                                OPAKPKTSNKKKGTKPKS-------ESVITSSNSTRSESELADS----SNPSGES
                                                                                                                                                                                QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑĄ;
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                                                                                                                                                                                                                                                                                                                                                                   48.4%; Score 661.5; DB 8
49.0%; Pred. No. 3.2e-55;
tive 25; Mismatches 66
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8
                                                                                                                                                                                                                                                                                                                                                                                                       Length 285;
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                                                                                                           ------FQIDDSFWSET 211
                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
   281
                                                                                                                                                                                      180
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the lectronic form from the US patent office at the polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme compositic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, recombination in plants, for improving yield by modification of plant or plants, for improving yield by modification of phonologous recombination in plants, for improving yield by modification of phonologous recombination in glants, for improving yield by modification of construct of the photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or physical and/or physical and/or physical construct of the plants of the used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 54105; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999;
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05-NOV-2001; 2001US-00985678.
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(KOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            improving
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d, heat, drought, herbicides, extreme osmotic conditions, pathogens
ts, for conferring increased resistance to plant disease, or for
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                          MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                             LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA
|:|||||||||||||||||
|LKPDIKRGNFTKEEEDAIISLHQILGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLE-DY
  QPAKPKTSNKKKGTKPKS---
                                                     QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                                                                                          MGRAPCCEKMGLKRGPWTPEEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yield.
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                                                                                                                                                                                                                                                                                                                                       Score 661.5; 1
Pred. No. 3.6e
25; Mismatches
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                                                                                   polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the sequence sequence them!?Doc!D:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of the cell cycle pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tole extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIUJ/)
(ZHOU/)
(KOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 40952; 15pp; English
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KOVALIC D K.
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CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou
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                                                                                                                                                                                                                                                                                                                                      Query Match 48.1%; Score 658; DB 8; Length 313; Best Local Similarity 46.6%; Pred. No. 8.1e-55; Matches 136; Conservative 34; Mismatches 64; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 313 AA;
                                                                                                           259 SITISNEMRLQYFFANYEETFQQGHHAYDSNFDDGMDFWYDIFTRTNDSIEL 310
                                                                         212 -----LSMPLDGYDVSMEPGDAFVAPPSADDMDYWLGVFMESGEAQDL 254
                                                                                                                                                                    155 -----LKSDQSKSKPSSKRAIKP-KIERSDSNS---SIITQSEPDNFNFREMD 198
                                                                                                                                                                                          121 QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS 180
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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transcription factor myb4 - barley (fragment)
c;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 31-Dec-2004
C;Accession: T05954

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-280 (ANI)
A;Cross-references: UNIPROT:Q02993; UNIPARC:UPI00000A6D7D; EMBL:Z13997; NID:g20560;
A;Cxoss-references: UNIPROT:Q02993; UNIPARC:UPI00000A6D7D; EMBL:Z13997; NID:g20560;
A;Experimental source: strain v26; developing flowers
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C;Keywords: DNA binding; duplication; nucleus; transcription regulation
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myb-related protein Ph2 - garden petunia
C;Species: Petunia x hybrida (garden petunia)
C;Date: 25-Feb-1994 #sequence_revision 03-Nov-1995 #text_change
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A;Experimental source: cv. Himalaya, endosperm
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A;Molecule type: mRNA
A;Residues: 1-288 <GUB>
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                       LRPDIKRGNFSKESEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD--A 118
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R;Coraggio, I.
R;Coraggio, I.
Submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: myb
C;Superfamily: Myb-related transcription activator; myb
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:004108; UNIPARC:UPI00000ACA8A; EMBL:Y11350; PIDN:CAA72185.1
A;Experimental source: cv. Arborio, coleoptile
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable myb-related protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision
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A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-276 <COR>
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                                  214 MPLDGYDVSME-PGDAFVAPPSADDMDYWLGVFMESGEAQDL
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                                                                                                                                    KLAAAGGG-----GGRRPHTRKQPKAAKSAAAVKREATPSVSVDTSSGVTCSTVTESS-P
                                                                                                                                                                      --APAQGGHVAASGGKK---HKKPKSAKKPAAA--AAAPPASPERSAS---SSVTESSMA 167
                                                                                                                                                                                                                                                                                                MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                        LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD---
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AGLGDMDEELAIAGTSSAAAARSDDMEFWLKMLLESGDMRDL
                                                                  SSADGDHRRQQQQTQHAAV---KEESFSSGGELPAAAAAPTAAADMDESFWSSTEVTGMM
                                                                                                    SSVAEEHGNAGISSASASVCAKEESSFTSASE-----EFQIDDSFWSET----LS
                                                                                                                                                                                                        LRPDIKRGNFTADEEDLIVRLHNSLGNRWSAIAAQMPGRTDNEIKNVWHTHLKKRLDDER
                                                                                                                                                                                                                                                                            MGRAPCCEKEGLRRGAWSPEEDDRLVAYIRRHGHPNWRALPKQAGLLRCGKSCRLRWINY
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                             51.0%; Score 697.5; DB 2; 53.2%; Pred. No. 1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DVTNDDQTFIKHEE----MDSYENFPEIDESFWTEDLSMG-DNL
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myb-related transcription factor THM18 - tomato ()Species: Lycopersicon esculentum (tomato) C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change C;Accession: T07395 F;Lin, O.; Hamilton, W.D.O.; Merryweather, A. Plant Mol. Biol. 30, 1009-1020, 1996 P;Title: Cloning and initial characterization of 14 myb-related A;Reference number: S69189; MUID:96270378; PMID:8639738 A;Accession: T07395 A;Accession: T07395 A;Roteus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-265 <LIN>

#text\_change 31-Dec-2004

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EMBL: X98308;

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A;Gene: myb1
C;Superfamily: Myb-related transcription activator; myb
C;Superfamily: Myb-related transcription regulation
C;Keywords: DNA binding; transcription regulation
F;9-61/Domain: myb DNA-binding repeat homology <MYB>
F;62-112/Domain: myb DNA-binding repeat homology <MYB>
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A;Experimental source: cultivar Ailsa Craig; hypocotyl
C;Genetics:
A;Gene: TIMI8
C;Superfamily: Myb-related transcription activator; myb
C;Keywords: DNA binding; transcription regulation
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB>
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Proc. Natl. Acad. Sci. U.S.A. 93, 14972-14977, 1996

A;Title: Isolation and characterization of a tobacco mosaic

A;Reference number: Z15119; MUID:97121500; PMID:8962166

A;Accession: T03850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                          LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD--A 118
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                                  PAQGGHVAASGGKKHKKPKS--AKKPAAAAA-----
                                                                                                                                              MVRAPCCEKMGLKKGPWIPEEDQILISFIQTNGHGNWRALPKQAGLLRCGKSCRLRWTNY
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   PPO--
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---NSKRHSKSKNHDSKGPTTSESSNNSDLTIINTQKHIDSPVLAPNSPQISS
                                                                                                                                                                                                                                     48.9%;
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                                                                                                                                                                                                                  Score 669.5; DB 2
Pred. No. 1.7e-42;
7; Mismatches 56
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                                                                     LGNRWSAIAAKLPGRTDNEIKNVWHTHLKKKLKDYK
                                                                                                                                                                                                                                                      DB 2;
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                                ----APPASPERSASSS
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C; Superfamily: 1
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A; Residues: 1-246 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
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Best Local
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                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q9LNC9; UNIPARC:UPI00000A8D57; GB:AE005172; NID:g8844123;
                                                                                                                117
                         226 GDAFVAPPSADDMDYWLGVFMES---
                                                                                                                                            121
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                                                                                                                                                                                                                                                                                             132;
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                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                            QGGHVAASGGKKHKKPKSAKKP--AAAAAAPPASPERSASSSVTESSMASSVAEEHGNAG
                                                                                                                                                                                        LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA
ND----KGYNHDMEFWFDHLTSSSCIIGEMSDISE
                                                                                ISSASASVCAKEESSFTSASEEFQ-IDDSFWSETLSMPLD-----
                                                                                                                -----HHSQDQNNKEDFVSTTAAEMPTSPQQQSSSSAD----ISAITTLGNNND
                                                                                                                                                                         LRPDIKRGNFTPHEEDTIISLHQLLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL----
                                                                                                                                                                                                                                   MGRRPCCEKIGLKKGPWSAEEDRILINYISLHGHPNWRALPKLAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                  MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STDHVMVAANQELQVQLPFSSF---KEENVDILATKMEDDMDFWYNVFIKTDDLPELPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEMSTVTLV-DDH-
                                                                                                                                                                                                                                                                                                                                                    Myb-related transcription activator; myb DNA-binding
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                         45.9%;
                                                      KDSATSSEDVLAI I DESFWSEVVLMDCDISGNEKNEKKIENWEGSLDR
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                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                        Score 628.5; DB 2; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                             Mismatches
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                         GEAQDLPQ 256
                                                                                                                                                                                                                                                                                                                     Length
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                                                                                   ----GYDVSMEP 225
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Maiti, R.;
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war, K.
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A;Description: The expre
A;Reference number: $712
A;Accession: $71283
A;Molecule type: DNA
A;Residues: 1-246 <KIR>
                                                                                                                     myb-related protein, 28K, leaf-specific - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change C;Accession: S71283
R;Kirik, V.; Koelle, K.; Misera, S.; Baeumlein. H.
                                                                                                        R;Kirik, V.; Koelle, K.; Mi
submitted to the EMBL Data
                                                                                                                                                                                                                                                        8
                                                                The expression mber: S71283
                                                                                                    K.; Misera, S.; Baeumlein,
L Data Library, August 1995
                                                                                    Library, Aug
                                                                                  leaf-specific
                                                                                                                                                                #text_change
                                                                                    myb
                                                                                  gene
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Θ
                                                                                                                                                                      31-Dec-2004
                                                                                      shifted to
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late embryo

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable MYB family transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: E84717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 45/1; 88/2
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat C;Keywords: DNA binding; duplication; nucleus; transcription regulation F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q39153; UNIPARC:UPI00000A0F29; EMBL:Z50869; NID:g1263092; A;Experimental source: strain Columbia C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-249 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84717
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                         Map position:
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181
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                                                                                                                                                                                                                                                                          Similarity 43.:
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRPDIKRGNFTPHEEDTIISLHQLLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                     NNG----
                                                                                                                                      LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                      MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ND----KGYNHDMEFWFDHLTSSSCIIGEMSDISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDAFVAPPSADDMDYWLGVFMES----GEAQDLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISSASASVCAKEESSFTSASEEFQ-IDDSFWSETL-----SMPLDGYDVSMEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGRRPCCEKIGLKKGPWSAEEDRILINYISLHGHPNWRALPKLAGLLRCGKSCRLRWINY
SASASVCAKEESSFTSASEEFQ---
                                                                            QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS 180
                                                                                                                   LRPDIKRGNFTPQEEQTIINLHESLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLSKNL
                                                                                                                                                                                               -----HHSODONNKEDFVSTTAAEMPTSPQQQSSSSAD----ISAITTLGNNND
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                                                                                                                                                                                                                                                                                              44.48;
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                                                                                                                                                                                                                                                                            38;
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Pred. No. 3.8
                                                                                                                                                                                                                                                                                              Score 608;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                              DB 2;
5.4e-38;
  ---IDDSFWSETLSMP-LDGYDVSMEPGDA
                                       ----GDTKDVNGINETTNEDKGSVIVD
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                                                                                                                                                                                                                                                                                                                                                        myb DNA-binding
                                                                                                                                                                                                                                                                                                               Length 249
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myb-related protein 1 - maize
N;Alternate names: myb-related protein Zml
C;Species: Zea mays (maize)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-2004
C;Accession: S04898
R;Marocco, A.; Wissenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, Mol. Gen. Genet. 216, 183-187, 1989
A;Title: Multiple genes are transcribed in Hordeum vulgare and Zea mays that car A;Reference number: S04896; MUID:89313655; PMID:2664447
A;Accession: S04898
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
S04898
                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P20024; UNIPARC:UPI000012FAD8
C;Superfamily: Myb-related transcription activator; myb DNA-binding repr
C;Keywords: DNA binding; duplication; nucleus; transcription regulation
F;11-63/Domain: myb DNA-binding repeat homology <MYB1>
F;64-114/Domain: myb DNA-binding repeat homology <MYB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 44/3; 88/3
C;Superfamily: Arabidopsis myb-related protein Y19; myb DNA-binding repeat homology C;Superfamily: Arabidopsis myb-related protein Y19; myb DNA-binding; duplication; nucleus; transcription regulation C;Keywords: DNA-binding repeat homology <MYB1>
F;9-61/Domain: myb DNA-binding repeat homology <MYB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myb-related protein Y19 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 C;Accession: S58294
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A; Residues: 1-122 < QUA>
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A; Residues: 1-340 < MAR>
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                                                                                                                                                                                        Local Similarity
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                                                                                 4 GRAPCCAKVGLNRGSWTPQEDMRLIAYIQKHGHTNWRALPKQAGLLRCGKSCRLRWINYL
                                                                                                              2 GRAPCCEKNGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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RPDLKRGNFTDEEEEAIIRLHGLLGNKWSKIAACLPGRTDNEIKNVWNTHLKKKV-
                        RPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPAQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGRAPCCEKMGLKRGPWTPEEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNY
                                                                                                                                                                       Conservative
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                                                                                                                                                                                        41.2%; Score 563.5;
49.4%; Pred. No. 1.6
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ibrary, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DDMDYWLGVFMES---GEAQDLPQ 256
                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 582; DB 1
Pred. No. 2e-36;
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                             .6e-34;
                                                                                                                                                                                                              DB 1;
                                                                                                                                                                       50;
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                                                                                                                                                                       Indels
                                                                                                                                                                                                            Length
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                                                                                                                                                                       Gaps
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myb protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence
C;Accession: T03828
                                                                                                                                                                                                                                        RESULT 13
T03828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.X.; Liuos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
submitted to the EMBL Data Librar;
A; Reference number: Z15103
A; Accession: T03828
A; Status: preliminary; translated
A; Molecule type: mRNA
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C; Superfamily:
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                                                                                                                   R; Coraggio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-274 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F309.29[imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         À;Cross-references: UNIPROT:Q9SA47; UNIPARC:UPI000009D685; GB:AE005172; NID:g4966369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Arabidopsis thaliana (mouse-
,Date: 02-Mar-2001 #sequence_revision
,Accession: D86300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                     221
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                                                                                                                                                                                                                                                                                                                                     QESEEDEVDKW 231
                                                                                                                                                                                                                                                                                                                                                                               APPSADDMDYW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASASVCAKEESSFTSASEE-----FQIDDSFWSETLSMPLDGYDVSMEPGDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNADEAGSKGSLNEEENSQE------SSPNASMSFA-----GSNISSKDDDAQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPDVKRGNFSAEEEDTIIKLHQSFGNKWSKIASKLPGRTDNEIKNVWHTHLKKRLSSETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRAPCCOKTKVKRGPWSHDEDLKLISFIHKNGHENWRSLPKQAGLLRCGKSCRLRWINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDAT-DVC----TLQPEDMDVSD-----MLVDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSMEPGDAFVAPPSADDM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                QMFEHILTYSE--FTGMLQEVDKPELLEMPFDLDPDIWSF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVT--ESSMASSVAEEHGNAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myb-related transcription activator; myb DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                               #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 562; DB 2;
45.4%; Pred. No. 1.6e-34;
ative 36; Mismatches 67
                                                                                             Library,
                             from GB/EMBL/DDBJ
                                                                                               February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-Mar-2001 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                -IDGSDSFQQPENRAL
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A;Status: processors in RNA
A;Molecule type: mRNA
A;Residues: 76-116,'Y',118-299 <KRA>
A;Residues: 76-116,'Y',118-299 <KRA>
A;Cross-references: UNIPARC:UPI00000AA8B8;
                                                                                                                                                                                                                                                                                            R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
T47917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T47917; T51638
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription factor MYB17 - Arabidopsis thaliana
N;Alternate names: protein T20K12.150
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: T47917; T51638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:004141; A;Experimental source: cv. Arborio, C;Genetics:
                                                                          A; Note: T20K12.150
C; Superfamily: Myb
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9M2D9; UNIPARC:UPI00000A65F8; EMBL:AL137898
A;Experimental source: cultivar Columbia; BAC clone T20K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-299 < DEH >
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C;Superfamily: Myb-related transcription
F;62-112/Domain: myb DNA-binding repeat h
                                                                                                                 A; Map position: A; Introns: 45/1;
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                                                                                                                                                            A;Gene: MYB17
                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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  Query Match
Best Local S
Matches 121
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 PALMQMASDASNLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 DILRIASAILPAATTTGAAAAAAABQAQLFIPWILQAQMAQQQQQVTPPPPPPPQAAATE
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h 39.9%;
Similarity 43.4%;
21; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RSASS---SVTESSMASSVAEEHGNAGISSASASVCAKEESSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGRAPCCEKSGLKKGPWTPEEDEKLIAYIKEHGQGNWRTLPKNAGLSRCGKSCRLRWTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFLQATS----TACHQMPGLVHASPTQQLAQQPQDHMAAATCHRRGAVQHPSYDNQLDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRPDIKRGRFSFEEEEAIIQLHSILGNKWSAIAARLPGRTDNEIKNYWNTHIRKRLLRMG
                                                                            Myb-related
                                                                                                                                          w
                                                                                                                     88/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.2%;
                                                                              transcription activator; myb DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat homology
                      Score 546;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - PREDEEDLTSELKPÄÄÄÄÄYYPTQADEDTERALEPEAGYP
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Pred. No. 1.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPARC: UPI00000AC830; coleoptile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator; myb
                                                                                                                                                                                                                    EMBL: AF062866; PIDN: AAC83588
                      DB 2;
?.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <MYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                H.D.; Denekamp, M.;
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A;Introns: 88/2
A;Introns: 88/2
A;Note: FSE19 110
C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-325 <SAT>
A;Cross-references: UNIPROT:Q9LFE1; UNIPARC:UPI00000AA6D3; EMBL:AL391147
A;Experimental source: cultivar Columbia; BAC clone F5E19
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                                                         LMVKTQIIDNPLDSFSSPIQPG
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                                                                                      FWSET--LSMPLDGYDVSMEPG 226
                                                                                                                                               ---PERSASSSVTESSMASSVAEEHGNAGISSASASVCAKEESSFTSASEEFQ---IDDS 206
                                                                                                                                                                            QMGIDPVT----HRPRTDHLNVLAALPQLIAAANFNSLLNLNQNVQLDATTLAKAQLLH 172
                                                                                                                                                                                                       QGGHVAASGGKKHKKPKS-----AKKPAAAAAPPAS------
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 532; DB 2; Length 325; 44.3%; Pred. No. 3.2e-32; ative 32; Mismatches 66; Indels
                2006, 00:04:35
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Sequence 11663, A
Sequence 11273, A
Sequence 10135, A
Sequence 8864, Ap
Sequence 8891, Ap
Sequence 33713, Ap
Sequence 26232, Ap
Sequence 26232, Ap
Sequence 11361, Ap
Sequence 11361, Ap
Sequence 1122, Ap
Sequence 11363, A
Sequence 10336, A
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Result No.

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
117.8	122.6	126.2	132.2	135.4	136.2	138.4	142.2	142.4	147	148.6	153.6	154.8	158	162.6	162.6	169	173	173	173.8
9.8	10.2	10.5	11.0	11.3	11.3	11.5	11.8	11.8	12.2	12.4	12.8	12.9	13.1	13.5	13.5	14.1	14.4	14.4	14.5
1426	1019	936	1575	1404	777	1680	1393	1421	1723	1584	1306	1101	1405	2412	2306	2142	2207	1894	2327
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US-10-953-349-24253	US-10-953-349-25118	US-10-953-349-5011	US-10-449-902-10076	US-10-449-902-18697	US-11-179-064B-75	US-10-449-902-9371	US-10-953-349-10214	US-10-449-902-28013	US-10-449-902-1432	US-10-953-349-30202	US-10-449-902-22352	US-10-953-349-16710	US-10-449-902-12272	US-10-449-902-6813	US-10-449-902-27399	US-10-449-902-6303	US-10-449-902-24194	US-10-449-902-3075	US-10-449-902-15504
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
24253, A	25118, A	5011, Ap	10076, A	18697, A	75, Appl	9371, Ap	10214, A	28013, A	1432, Ap	30202, A	22352, A	16710, A	12272, A	6813, Ap	27399, A	6303, Ap	24194, A	3075, Ap	15504, A

## ALIGNMENTS

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Sequence 11663

(Sequence 11663, Application US/10449902)

(Sequence 1163, Application US/10449902)

(Publication No. US20060123505A1)

(GENERAL INFORMATION:

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

(TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

(CURRENT APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-2038970

PRIOR APPLICATION DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SEQ ID NO 11663

TVDE. DN3

LENGTH: 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: OTYZA SATIVA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK109011
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11663
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 380; Conser
                                                                                                                                                                                                                                                                                                           77 CAATGGGGAGGGCTCCGTGCTGCCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGG
                                                                                                                                                                                                           AGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCC
ACCTGCGGCCGGACATCAAGCGGGGGAACTTCTCCAAGGAGGAGGAGGAGGACACCATCATCC
                                                                                                                                                                           CGATGGGGAGGCGCCGTGCTGCGAGAAGGAGGGGGCTGAGGAGAGGGGGGCGTGGAGCCCCG
                                                                                                  TGCCCAAGCAAGCCGGGCTGCCTGCGCTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACT
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Pred. No. 7.7e-51;
0; Mismatches 153;
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421 403

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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institutior APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-303870

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11273

LENGTH: 1399
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Best Local S
Matches 446
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                                                                                                                                                                                                                                                                                                                                                                     -10-449-902-11273
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: OTYZA BATİVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK100
DATABASE ENTRY DATE: 2002-08-28
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                                                                                                         GCAACTGGCGCGCCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGC
                                                                                                                                            GGCCGTGGACGCCGGAGGACAAGCTCCTCGTCGACTACATCCAGGCCAACGGCCACG
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 TGCGGTGGACGAACTACCTCCGGCCGGACATCAAGCGCGGGCCCTTCACCGCCGAGGAGC
                              TCCGGTGGATCAACTACCTGCGGCCGGACATCAAGCGGGCCAACTTCTCCAAGGAGGAGG
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                                                                                                                                                                                                                                                                                                              Score 251.8; DB 6
Pred. No. 5.5e-47;
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                                                                         283
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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER: OF SEO ID NOS: 56791

COLUMBER OF SEO ID NOS: 56791
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US-10-449-902-10135
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                                                                            Matches
                                                                                            Query Match
Best Local
                                                                                                                                                                   ORGANISM: Oxyza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107483
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                               LENGTH: 1163
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                                                                                            Similarity
                            ATGGGGAGGCTCCGTGCTGCGAGAAGATGGGGCTCAAGAAGGGTCCATGGACGCCGGAG
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     ATGGGGAGGCAGCCGTGCTGCGACAAGGTGGGGCTGAAGAAGGGGGCCGTGGACGGCGGAG
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                                                                            Conservative
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                                                                                              Score 248.2;
Pred. No. 3.2
                                                                            ed. No. 3.2e-46;
Mismatches 243
                                                                                                                 DB 6;
                                                                              243;
                                                                              Indels
                                                                                                               Length 1163;
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823 766 706 703 646 643 586 583 526 523 466 463

763

12;

Gaps

138

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GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5864
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US-10-449-902-5864
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         TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK063027
DATABASE ENTRY DATE: 2001-12-06
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                                                                                                                                                                          SOFTWARE: PatentIn Ver.
SEQ ID NO 8691
LENGTH: 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8691, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
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Matches
                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institu
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
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Best Local (
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                     PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK10
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                             LENGTH:
                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
                Local Similarity
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              Score 223.6; DB 6;
Pred. No. 8.7e-41;
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Pred. No. 1.1e-41;
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 Mismatches
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33713
LENGTH: 1284
TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (736)...(736)
OTHER INFORMATION: n is a, c, 9
US-10-953-349-33713
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US-10-953-349-33713
Sequence 33713, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                          CCCTGCCCAAGCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCA
                                                                                                             CGATGGGGCGGTCGCCGTGCTGCGAGAAGGAGGCCGGGCTGAAGAAGGGGCCGTGGACGT
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ACTACCTGCGGCCGGACATCAAGCGGGGCAACTTCTCCCAAGGAGGAGGAGGACACCATCA
                                                                                           CCGAGGAGGACCAGAAACTGCTGGCCTTCATCGAGCACGGACACGGCTGCTGGCGCT
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                               CGCTGCCGGCTAAGGCCGGTCTGCGGCGGTGCCGAAGAGCTGCCGGCTCCGGTGGACCA
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Pred. No. 1.4e-40;
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JD 2002-203269
PRIOR APPLICATION NUMBER: JD 2002-303870
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JD 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARR: PRECENTIN Ver. 2.1
SEQ ID NO 7552
LENGTH: 1389
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US-10-449-902-7552
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Best Local S
Matches 267
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK064679
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 18.1%;
Local Similarity 76.5%;
les 267; Conservative
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TCTCCACGAGCTGCTTGGCAACAGGTGGTCCGCCAATTGCCGCCAGGTTGCCCGGGAGGAC
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                                                                                    CCTGCACGAGCAGCTCGGCAACAGGTGGTCCAAGATCGCGTCGCACCTGCCGGGCAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 217.8; DB 6; Pred. No. 1.8e-39; 0; Mismatches 82;
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RESULT 4 US-10-49-902-2899 ; Sequence 2899, Application US/10449902 ; Publication No. US20060123505A1

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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
TITLE REFERENCE: MOA-A020SY1-US
CURRENT APPLICATION, NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2899
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Matches 389; Conserv
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ORGANISM: Oryza Bativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK060684
DATABASE ENTRY DATE: 2001-12-06
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CCGCGGTGCCCCGACCTCAACCTCGACCTCGACCTGTCCATGAGCCTG
                                  GAGGAGTTCCAGATCGACGACAGCTTCTGGTCGGAGACGCTGTCGATGCCGCTG 726
                                                                                                            ATCAGCTCGGCGTCCGCGTGTGCGCCAAGGAGGAGCTCCTTCACCTCGGCTTCC
                                                                            TCCGCGGCGTCCCCGCCGTCGGAGGACGGCCACAGCAGCAGCCGGCGGCAGCTCGGACGCG
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Pred. No. 1.8e-39;
0; Mismatches 259;
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750
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Sequence 3902, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: Foundation for Advancement of International Science.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR PILING DATE: JO2020-383870
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 26232
LENGTH: 995
TYPE: DNA
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PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK10:
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26232
                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-10-449-902-3902
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
APPLICANT: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A032051-US
FULL REPERENCE: MOA-BOSS1-US/10/449,902
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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Pred. No. 1.9e-39;
D; Mismatches 81
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Institution

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Sequence 11361, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: Poundation for Advancement of Agrobiological Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF.

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: 309-05-30

PRIOR APPLICATION NUMBER: 309-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER: DATE: 2002-12-11

NUMBER: DATE: 2002-12-11
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NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PATENTIN Ver. 2:1
SEQ ID NO 3902
LENGTH: 1087
TYPE: DNA
OTYPE: DATABASE ENTRY DATE: 2001-12-06
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US-10-449-902-11361
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                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 11361
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TYPE: DNA
ORGANISM: OTYZA SALİVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK100
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                          LENGTH: 1031
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Pred. No. 2.4e-39;
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-0A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION UNMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER: DATE: 2002-12-11
SOFTMARE: PatentIn Ver. 2.1
SOFTMARE: PatentIn Ver. 2.1
SEQ ID NO 1122
LENGTH: 1042
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US-10-449-902-1122
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Best Local S
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104053
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Pred. No. 2.5e
0; Mismatches
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Pred. No. 9.4e-38;
0; Mismatches 192;
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TGCCCAAGGCGGCGGCCTCCTTCGCTGCGGCAAGAGCTGCCGCCTCCGGTGGATGAACT

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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A020571-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-2038970
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
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US-10-449-902-16336
                                                                                                                                                                                                                                                                                                                                US-10-449-902-16336
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                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1069
TYPE: DNA
ORGANISM: OYZB BBTIVB
ORGANISM: OYZB BBTIVB
DATABASE ACCESSION NUMBER: AK066834
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                  Local Similarity
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                                      TGCCCAAGCCAAGCCGGGCTGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACT
                                                                                                                      AGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCC
                                                                                                                                                             CCATGGGGAGGTCGCCGTGCTGCGAGAAGGCGCGCACACGAACAAGGGGGGCGTGGACGAAGG
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Pred. No. 9.5e-38;
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US-10-449-902-19393
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SEQ ID NO 19393
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-303870
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ ID NOS: 56791
NUMBER: OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                               LENGTH: 1023
TYPE: DNA
ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099108
DATABASE ENTRY DATE: 2002-08-28
261
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                                                                                                           AGGAGGACAAGGTCCTCGTCGCCCACATCCAGCGCCACGGCCACGGCAACTGGCGCGCCC
                                                                                                                                                               CCATGGGGAGGTCGCCGTGCTGCGAGAAGGCCGCACACGAACAAGGGGGGCGTGGACGAAGG
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                                        TGCCCAAGCAAGCCGGGCTGCCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACT
                                                                                 AGGAGGACCAGCGGCTCATCGCGTACATCAGGGCGCATGGCGAAGGCTGCTGGCGCTCGC
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                                                                                                                                                                                                                                            Score 208.2; DB 6;
Pred. No. 2.1e-37;
0; Mismatches 193;
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APPLICANT: Bio-oriented Technology Research Advancement Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

ITITLS OF INVENTION: FULL-LENOTH PLANT cDNA AND USES THEREOF FILE REFERENCE: MOA-0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF ESO ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: DNA

ORGANISM: OTYZA SATIVA

DATABASE ACCESSION NUMBER: AK104457

DATABASE ENTRY DATE: 2002-08-28
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Best Local Similarity
Matches 257; Conserv
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                       CCCAAGCAAGCCGGGCTGCGTTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
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 Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*

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                    Sequence 122749,
Sequence 272820,
Sequence 343620,
Sequence 4, Appli
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Sequence 25633, A
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Sequence 33593,
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Sequence 211042, A
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Sequence 12004, A
Sequence 1472, A
Sequence 2475, A
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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	822, App	22, Appl	267017,	ທ	38, Appl	38, Appl	<ol><li>Appli</li></ol>	776, App	1754, Ap	164, App	156, App	1978, Ap	40, Appl	776, App		140, App	62, Appl	

## ALIGNMENTS

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OTHER INFORMATION: Clone ID: PAT_MRT4530_25649C.1.pep US-10-437-963-122749
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122749
LENGTH: 257
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1368; DB 4; Length Best Local Similarity 100.0%; Pred. No. 8.2e-113; Matches 257; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andr
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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WIGVEMESGEAQDIPQI 257
                                            SASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSMEPGDAFVAPPSADDMDY
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Sequence 343620, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 343620
LENGTH: 279
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules a
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FULL REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 222820
LENGTH: 295
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US-10-425-115-222820
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Best Local Similarity
                                                   TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(279)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                   236 MPLDSLDDVVPMEPSDDAFGDVDVDVAAASSSSVGADGDLDYWLRVFMESGDAHPELPQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKKLDAPA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPLDGYD--VSMEPG-DAF----VAPPSAD-----DMDYWLGVFMESGEAQ-DLPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AASSSVTESSMTEQ-EQEHGNTGSSPA----FPKEESLTTSSSDAEEFQFDDSFWSETLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ASSSVTESSMASSVAEEHGNAGISSASASVCAKEESSFTSAS--EEFQIDDSFWSETLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEQQQQHGTTPAAGAGKKHRPAAAAKRGGGGARKATANADAVVVPAPAPATAAPASPERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRPDIKRGNFSKEEEDAIISLHEQLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDPTK
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Pred. No. 5.2e-73;
"""matches 41; Indels 48;
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                                                                                                                                                                                                                             Other Molecules Associated With
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     WS-09-443-704-4
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Sequence 10942, Application US/11087099
PUBLICATION NO. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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US-11-087-099-10942
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LENGTH: 288
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Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 61.1%; Score 835.5; DB 6; Local Similarity 64.7%; Pred. No. 1.6e-65;
                                                                                                                                                                                    136 PKSAK-------KPAAAAAAPPASPERSASSSVTES-SMASSVAEEHGN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 MASSVAEEHGNAGISSASASVCAKEESSFTS---ASEEFQIDDSFWSETLSMPLDGY-DV
253 G--DMDYWLRLFMEGGGGSGSGSDDNNNHDGALDLPQI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 PTEPCSSGAFGDVAASSSSSSSGADADLDYWLGVFMKSGDAHQQLPQV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 Q-----PASPERS-ASSSVTESS 165
                                                                                                                                                                                                                                                                                                                                                                        61 LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                74 QSIIQLHQLLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDPSAQEQQEEAGAAKKRKK 133
                                                                                                                                                                                                                                                                                                                            76 DTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPAQGGHVAASGGKKHKK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LRPDIKRGNFSKEEEDAIITLHEQLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLEPTT
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                                                                                                                    AGISSASASVCAKEESSFTSA--SEEFQIDDSFWSETLSMPLDGY-DVSMEPGDAFVAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQLEQEQHGAHAGGDAARKRSRPKRAGARXKTTTAAVAPATTAPASPERSAASSSVTEST
                                              SADDMDYWLGVFMESG-----
                                                                                            SGSSSASASASVKEE-CFTSSEESEEFQIDESFWSETLSMPLDDLNDVCMEPHDAFGKPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                              ---EAQDLPQI 257
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Sequence 4, Application US/09443704

Patent No. US20020066120A1

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Liu, Zhan-Bin
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
ITITE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: NO. US20020066120Alember 20, 1998
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 258
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US-10-008-118A-4
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, ORGANISM: Oryza sativa
US-09-443-704-4
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Best Local Simi
Matches 169;
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10008118A Publication No. US20020187539A1 GENERAL INFORMATION:
                                                                                                                      SOFTWARE: Microsoft Office 97
SEQ ID NO 4
Query Match 60.5%; Score 827.5; DB 4; Best Local Similarity 62.1%; Pred. No. 6.9e-65; Matches 169; Conservative 29; Mismatches 45;
                                                                                                                                                    APPLICANT: Cahoon, Rebecca E.
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription
FILE REFERENCE: BB1280 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/109,294
PRIOR FILLNG DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
                                                            LENGTH: 258
TYPE: PRT
ORGANISM: Oryza sativa
-10-008-118A-4
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                                                                                                                                                                                                                                                                                                                                                                                                              GASPSSSNDDDMDDFWLKLFIQAGGMQNLPQI
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                             Length 258;
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Go, Yongwei
APPLICANT: Boukharov, Andre:
APPLICANT: Batbazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 204966; SEQ ID NO 192931
LENGTH: 258
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-437-963-192931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT4530_89117C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 60.5%; So
Local Similarity 62.1%; Pi
hes 169; Conservative 29;
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                                                                                                                                               121 SSGREAAA-----PKRKATKKAAAVAVAIDVPTTVPVSPEQSLSTTTT----SAATTEBY
                                                                                                                                                                                                                                                                          61 LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LRPDIKRGNFTREEEDAIIHLHDLLGNRWSAIAARLFGRTDNEIKNVWHTHLKKRLEPKP 120
                                                                                                                                                                                                                                                                                                                                      1 MGRAPCCEKMGLKRGPWTAEEDRILVAHIERHGHSNWRALPRQAGLLRCGKSCRLRWINY
VAPPSA---DDM-DYWLGVFMESGEAQDLPQI
                                                  SYSMASSADHNT----TDSFTS-EEEFQIDDSFWSETLAMTVDSTDSGMEMSGGDPLGAG
                                                                                  GNAGISSASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSME-----PGDAF
                                                                                                                                                                   QGGHVAASGGKKHKKPKSAKKPAAAAAA------PPASPERSASSSVTESSMASSVAEEH 174
                                                                                                                                                                                                                                            LRPDIKRGNFTREEEDAIIHLHDLLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLEPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGREAAA-----PKRKATKKAAAVAVAIDVPTTVPVSPEQSLSTTTT----SAATTEEY 171
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US-11-096-568A-25633
Sequence 25633, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA F
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592US2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25633
LENGTH: 257
TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                             APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA F
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25632
LENGTH: 309
TYPE: PRT
CENTIED: Zea mays subsp. mays
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US-11-096-568A-25632
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, NAME/KEY: misc feature
; LOCATION: (1)..(257)
; OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-25633
                                                                       ; FEATURE: misc feature
; NAME/KEY: misc feature
; LOCATION: (1)..(309)
; OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-25632
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Query Match
Best Local Similarity
Matches 160; Conserv
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Best Local Similarity
Matches 160; Conserv
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 58.4%; Score 799.5; DB 6;
58.8%; Pred. No. 2.7e-62;
tive 30; Mismatches 51;
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                                    Length 309;
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US-10-425-115-335937
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335937
LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 157; Conserv
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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GKSAAAPSSTNDDMDFWLKLFMQASDMQNLPQI
                                                                                                    EHGNAGISSASASVCAKEESSFTSASEEFQIDDSFWSETLSM--PLDGYDVSMEP-----
                                                                                                                                                                                                                                                                               MGRSPCCEKMGLKRGPWTAEEDRILVAHVERHGHSNWRALPKXQAGLLRCGKSCRLRWIN
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                                                                                                                                     PASQQAPKRKPTKKQQPQPEPEPVTTLEGPÅGÅVPPVSPERSLSTTTSTTTSTADYSAAS
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;; Pred. No. 7.3e-62;
31; Mismatches 56
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                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)..(248)
; OTHER INFORMATION: Ceres
US-11-096-568A-25634
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US-11-096-568A-25634
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US-10-425-115-237771
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated I
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 237771
TYPE. DET
                                                                                                                                                            APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25634
LENGTH: 248
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Query Match
Best Local Similarity
Matches 152; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                       DDMDYWLGVFMESGEAQDLP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSMEPGD-AFVAPPSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASSSL--ENADSFTSEEEDYQIDDSFWSETLAMAVDSSDSGMEEAEGAFGASPPAPSTN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TATQAPK-RKPKKQQQPEAVTLAAPVSPEQSAVSTSTTST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGRAPCCEKKGLRRGAWSPEEDQRLVAYVRQNGHPNWRALPQQAGLPRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS 180
   54.6%; ilarity 57.8%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%; Score 769; DB 4; Length 241; 57.7%; Pred. No. 9.8e-60;
                                                                        seq.
    29;
   Score 747.5; DB 6;
Pred. No. 8.2e-58;
9; Mismatches 51;
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    Indels
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                              248;
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   Gaps
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Sequence 1043, Application US/11087099
PUBLICATION NO. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID.NO 1043
                                                                                                                                                     US-10-767-701-42619
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; TYPE: PRT
; ORGANISM: Petunia
US-11-087-099-1043
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US-11-087-099-1043
Sequence 42619, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                                            225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAQGGHVAASGGKKHKKPKSAK-------KPAAAAAAPPASPERSA--SSS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRPDIKRGNFTREEEDTIIQLHEMLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLKNYQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGRAPCCEKMGLKKGPWTPEEDQILVSYIEKNGHGNWRALPKLAGLLRCGKSCRLRWTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD-APAQGGHVAAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                      PPQNSKRHSKNNHDSKAPSTSKMLDNSESFSTIQENINEPMTG----PNSPQRSSSESST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 6;
2.2e-54;
nes 55;
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Sequence 110426, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NO 110428
LENGTH: 276
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_14495C.1.pep
US-10-437-963-110428
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C81473_1.pep
US-10-767-701-42619
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CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42619
LENGTH: 200
TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.0%;
                                                                                                                                         Matches 150;
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Best Local (
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                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                  y Match
Local Similarity 53.2%;
hes 150; Conservative 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPEEQHGAQAGGAGKKHRPKRGAAKKTTADDVAVVPATTAPVSPERSPASSSVTESSSMT 180
                                                                                       MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
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                                                                                                                                       ; Score 697.5; DB 4;
; Pred. No. 2.5e-53;
34; Mismatches 61;
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                                                                                                                                                                             Length 276;
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232 AGLGDMDEELAIAGTSSAAAARSDDMEFWLKMLLESGDMRDL 273
                                                                                                                                                                                            118 --APAQGGHVAASGGKK---HKKPKSAKKPAAA--AAAPPASPERSAS---SSVTESSMA 167
                    MPLDGYDVSME-PGDAFVAPPSADDMDYWLGVFMESGEAQDL 254
                                                                        SSADGDHRRQQQQTQHAAV---KEESFSSGGELPAAAAAPTAAADMDESFWSSTEVTGMM 231
                                                                                                                 SSVAEEHGNAGISSASASVCAKEESSFTSASE-----EFQIDDSFWSET----LS
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Search completed: June 24, Job time : 187 secs 2006, 00:08:43

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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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| MMC_Celerra_SIDS3/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*
| EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
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Sequence 40114, A Sequence 2592, Ap Sequence 22501, A Sequence 2701, Ap Sequence 37024, A Sequence 34326, A Sequence 34326, A Sequence 34326, A Sequence 343274, A Sequence 44751, A Sequence 47791, A Sequence 10215, A Sequence 10215, A Sequence 33817, A Sequence 39812, A Sequence 31811, A Sequence 31814, A Sequence 31840, A Sequence 5012, Ap
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US-10-449-902-40114
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27.8	27.8	27.9	28.8	28.8	29.4	29.5	29.5	29.8	29.9	29.9	30.3	30.8	31.8	32.9	33.1	33.9	33.9	34.7	34.8
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ALIGNMENTS

## Sequence 40114, Application US/10449902 | Publication No. US20060123505A1 | GENERAL INFORMATION: | APPLICANT: National Institute of Agrobiological Sciences. | APPLICANT: Bio-oriented Technology Research Advancement Institution APPLICANT: The Institute of Physical and Chemical Research. | APPLICANT: Foundation for Advancement of International Science. | APPLICANT: Foundation for Advancement of International Science. | APPLICANT: Foundation for Advancement of International Science. | TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US | CURRENT APPLICATION NUMBER: US/10/449,902 | CURRENT APPLICATION NUMBER: US/10/449,902 | CURRENT FILING DATE: 2003-05-29 | PRIOR APPLICATION NUMBER: JP 2002-203269 | PRIOR APPLICATION NUMBER: JP 2002-383870 | PRIOR APPLICATION NUMBER: JP 2002-383870 | PRIOR APPLICATION NUMBER: US/10/449,902 | PRIOR APPLICATION NUMBER: JP 2002-383870 | PRIOR FILING DATE: 2002-11-11 | NUMBER: OF SEQ ID NOS: 56791 | SEQ ID NO 40114 | LENGTH: 276 | TYPE: PRT | COLUMENT | ; ORGANISM: Oryza sativa US-10-449-902-40114 Query Match 51.0%; Score 697.5; DB 6 Best Local Similarity 53.2%; Pred. No. 8.3e-44; Matches 150; Conservative 34; Mismatches 61 232 AGIGDMDEELAIAGTSSAAARSDDMEFWLKMLLESGDMRDL 273 214 MPLDGYDVSME-PGDAFVAPPSADDMDYWLGVFMESGEAQDL 254 121 KLAAAGGG-----GGRRPHTRKQPKAAKSAAAVKREATPSVSVDTSSGVTCSTVTESS-P 118 --APAQGGHVAASGGKK---HKKPKSAKKPAAA--APAPPASPERSAS---SSVTESSMA 167 1 MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 1 MGRAPCCEKEGLRRGAWSPEEDDRLVAYIRRHGHPNWRALPKQAGLLRCGKSCRLRWINY SSADGDHRRQQQQTQHAAV---KEESFSSGGELPAAAAAPTAAADMDESFWSSTEVTGMM SSVAEEHGNAGISSASASVCAKEESSFTSASE-----EFQIDDSFWSET----LS 61; . 6 Indels Length Institution. 276; 37; Gaps 231 120 213 174 117 60 60

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Sequence 22502, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA-
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOPTWARE: Patentin version 3.3

SEQ ID NO 22502

LENGTH: 275
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIN version 3.3
SEQ ID NO 9699
LENGTH: 285
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
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Best Local (
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-10-953-349-22502
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                             MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
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   MVRAPCCEKMGLKKGPWAPEEDQILTSYIDKHGHGNWRALPKQAGLLRCGKSCRLRWINY
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49.0%; Pred. No. 3.5e-41;
ative 25; Mismatches 66
                                                                                           46.6%;
                                                                         Score 658; DB 6
Pred. No. 6e-41;
4; Mismatches
                                                                                                             DB 6; Length 275;
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APPLICANT: ALEXANDROV, Nickolai et al.
FAPILICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22501
LENGTH: 320
TYPER: PRT
ORGANISM: Glycine max
US-10-953-349-22501
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US-10-953-349-22503
; Sequence 22503, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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            APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                  206 TITSSACTTSSSDFSSVTVGDSKNIKSEDTESTETMPVIDESFWSEAAIDDETPTMSSSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 LRPDIKRGNFTIEEEETIIKLHDMLGNRWSAIAAKLPGRTDNEIKNVWHTNLKKRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 SLTISNEMRLQYPFANYEETFQQGHHAYDSNFDDGMDFWYDIFTRTNDSIEL
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SEQ
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ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.1%; Score 658; DB 6;
46.6%; Pred. No. 7.1e-41;
ative 34; Mismatches 64
                                                                                                  DNA
                                                                                                    FRAGMENTS
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                                                                                                    CORRESPONDING POLYPEPTIDES
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US-10-953-349-9700
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US-10-953-349-22503
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9700
LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 137; Conserv
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SEQ ID NO 22503
LENGTH: 266
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Best Local S
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VS-----MEPGDAFVAPPSAD------DMDYWLGVFMESGEAQDL 254
                                                                                                                                                                                              GKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGISSASASVCAK 189
                                                                EVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKETLYSQDEHNY
                                                                                                                                                                                                                                 EESSFTSASEE----
                                                                                                                                                   KKKGTKPKS-----ESVITSSNSTRSESELADS----SNPSGESLFSTSPSTS
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ilarity 45.2%;
Conservative 3
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Pred. No. 1.2e-37;
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                                                                                                         - FQIDDSFWSETLSMPLDGYD
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US-10-449-902-38592
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SEQ ID NO 38592
LENGTH: 267
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Publication No. US20060123505A1
                                   APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical Michemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A020SY1-US
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UF 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PRIOR DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 203-05-29
                      SOFTWARE: PatentIn Ver.
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PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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Local Similarity 43.3%; Pred. No. 1e-32;
les 117; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGAGVDVDVDVDFFDHYYHDASFDDQDVWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRPDLKRGLLSDDEERLVIDLHAQLGNRWSKIAARLPGRTDNEIKNHWNTHIKKKLRKMG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAAAAEAATSNCSVSPASVLSPSCSSSASAASAVDVAEWPEPMYMFGMDGIMDVGWNGLI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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32;

Gaps

s

60

SSQP----SSPPPPPHEAEARRAGATASYTYHHHYSETREKICLCLNHLGLHGGDECSCG 236

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Sequence 34326, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

TITLE OF INVENTION NUMBER: US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-303870

PRIOR APPLICATION NUMBER: JP 2002-303870

PRIOR APPLICATION DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SEQ ID NO 34326

LENGTH: 266
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; TYPE: PRT
; ORGANISM: Oryza :
US-10-449-902-39724
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US-10-449-902-34326
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Best Local Similarity
Matches 118; Conserv
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Best Local S
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TYPE: PRT
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             AKKPAAAAAAPPASPERS----ASSSVTESSMASSVAEE---
                                                       LDPLTHRPLNAAAAVAGHHHLAAGGSSCSPDATSGHSSCSDGDEYRGGIDLNLSISPPSS
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                                                                                                                                                        LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDA---
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                                                                                                                                 LRPDLKRGNFTDEEDELIIKLHELLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLARG
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Pred. No. 2.9e-31;
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US-10-953-349-33714
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Matches
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
                                                                                                                                                                             Sequence 29589, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
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              APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
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NAME/KEY: misc feature
LOCATION: (204)...(204)
OTHER INFORMATION: Xaa
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Llarity 36.9%;
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Pred. No. 4.4e-31;
4; Mismatches 68
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PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44757
LENGTH: 260
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US-10-449-902-44757
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US-10-449-902-29589
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PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29589
LENGTH: 260
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US-10-449-902-44757
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Best Local Similarity
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                                                                                                                                                                                                                                                Matches
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APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A020511-US
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CURRENT FILING DATE: 203-05-29
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IDPQTHRPLLSGGDGIAASNKAAPPPPHPISVPAKAAAAAIFAVAKPPPPPRPVDSSDDG
                                                                                                    LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAP- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAP- 119
                                                                                                                                                             MGRS PCCEKAHTNKGAWTKEEDQRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDPQTHRPLLSGGDGIAASNKAAPPPPHPISVPAKAAAAIFAVAKPPPPPRPVDSSDDG
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                                                                              LRPDLKRGNFTDDEDELIIRLHSLLGNKWSLIAGQLPGRTDNEIKNYWNTHIKRKLLARG
                                                                                                                                                                                                                                            37.4%; Score 511; DB 6; I ilarity 52.1%; Pred. No. 2.5e-30; Conservative 22; Mismatches 50;
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52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 511; DB 6;
Pred. No. 2.5e-30;
                                                                                                                                                                                                                                                                                       DB 6; Length 260;
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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 32367
LENGTH: 311
TYPE: PRT
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US-10-449-902-47791
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR PPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
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US-10-449-902-47791
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32367, Application US/10449902
Publication No. US20060123505A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
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RESULT 15
US-10-953-349-10216
US-10-953-349-10216
Sequence 10216, Application US/10953349
Publication No. US20060107345A1

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOUTHWARE: PatentIn version 3.3
SEQ ID NO 10216
LENGTH: 342
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-10216
Search completed: June 24, Job time : 23 secs
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US-10-449-902-32367
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                                                                                                                  165 SMASSVAEEHGNAGISSASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSME
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                                                                                                                                                          AVSGDGHNLLVNDVVLKKSCSSSSGAKNNNKTKKKKK----
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                                                                                K------QMVTASQCFSQPKELESDFSEGGQNGNFEGESLG-PYEWLDGELE
                    2006, 00:09:11
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1368
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| / EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/6_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/7_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/RE_COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                      US-08-722-626B-2

US-09-533-029-112

US-09-540-211A-2151

US-09-640-211A-2251

US-09-640-211A-2251

US-09-640-211A-2271

US-09-640-211A-2271

US-09-640-211A-2201

US-09-640-211A-1093

US-09-640-211A-2210
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Sequence 2, Appli
Sequence 62, Appl
Sequence 112, Ap
Sequence 2161, Ap
Sequence 2161, Ap
Sequence 2259, Ap
Sequence 2259, Ap
Sequence 2277, Ap
Sequence 2101, Ap
Sequence 2101, Ap
Sequence 672, Appli
Sequence 672, Appli
Sequence 238, Ap
Sequence 94, Appli
Sequence 94, Appli
Sequence 2260, Appli
Sequence 1093, Ap
Sequence 2260, Appli
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Sequence 1093, Ap
Sequence 2248, Ap
Sequence 2248, Ap
Sequence 2248, Ap
Sequence 2249, Ap
Sequence 2240, Ap
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         US-08-722-626B-2
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381	387.5	390	390.5	398	404	408	413.5	427	427	438	440.5	445	449	450	450	456	459	459.5
27.9	28.3	28.5	28.5	29.1	29.5	29.8	30.2	31.2	31.2	32.0	32.2	32.5	32.8	32.9	32.9	33.3	33.6	33.6
224	168	148	208	107	101	112	175	146	128	109	119	113	107	107	107	126	226	226
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US-09-640-211A-919	US-09-640-211A-2245	US-09-640-211A-2206	US-09-640-211A-2250	US-09-640-211A-1118	US-09-640-211A-2169	US-09-640-211A-1112	US-09-640-211A-2159	US-09-640-211A-2215	US-09-640-211A-1083	US-09-640-211A-2141	US-09-640-211A-1082	US-09-640-211A-1099	US-09-640-211A-2230	US-09-640-211A-2244	US-09-640-211A-2156	US-09-640-211A-2139	US-09-453-387A-4	US-09-640-211A-2256
Sequence 919, App	•	•	Sequence 2250, Ap	•	2169,	Sequence 1112, Ap	2159,	2215,	1083,	2141,	1082,	Sequence 1099, Ap	2230,	Sequence 2244, Ap	•		.⊠	Sequence 2256, Ap

ALIGNMENTS

## S-08-722-626B-2 Sequence 2, Application US/08722626B Patent No. 5939601 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION GENERAL INFORMATION: GENERAL TYPE: DISCIPLING GENERAL INFORMATION: GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION GENERAL INFOR

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APPLICANT: APPLICANT: APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: MISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
LENGTH: 273
TYDE: DET
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                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Arabidopsis thaliana; FEATURE: OTHER INFORMATION: G233
US-09-533-029-62
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US-09-533-029-62
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 132; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Ratciffe, Oliver
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
121 QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 STDHVMVAANQELQVQLPFSSF---KEENVDILATKMEDDMDFWYNVFIKTDDLPELPE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LKPDIKRGNFTKEEEDAIISLHQILGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLE-DY 119
                                                                              61
                                                                                                                            LRDDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------MPLDGYDVSMEPGDAFVAPPSADDMDYWLGVFMESGEAQDLPQ 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPQ-----NSKRHSKSKNHDSKGPTTSESSNNSDLTIINTQKHIDSPVLAPNSPQISS 173
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                                                                                                                                                                                                             46.8%; Score 640; DB 2; Length 273; ilarity 54.8%; Pred. No. 4.8e-58; Conservative 19; Mismatches 44; Indels
                                                                                                                                                                                                                    44; Indels 46;
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	CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16		
	INVENTION: Compositions and Methods for the INVENTION: Modification of Gene Transcription		
	McGrath, Annette Glenn, Matthew	777	
	ORMATION: Wood, Marion Shenk Michael	GENERAL APPLICA	
	211A-2161 2161, Application US/09640211A o. 6833446	S-09-640- Sequence Patent N	
	1 LRPDIKRGNESKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLD 117	n 0	
60	1 MGRAPCCEKMGLKRGPWTPBEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNY	Db	
60	1 MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY	Qy	_
0	ch 42.5%; Score 582; DB 2; Length 122; 1 Similarity 85.5%; Pred. No. 1.5e-52; 100; Conservative 11; Mismatches 6; Indels 0; Gaps	Query Match Best Local Matches 10	
	INFORMATION: G241 029-112	); OTHER INF	<b>a.</b> .
	: Arabidopsis thaliana	ORGANISM:	
	112 122	SEQ ID NO	
	SEQ ID NOS: 121 Patentin Ver. 2.1	UMBER C	
	FILING DATE: 2000-03-72 APPLICATION NUMBER: 60/125,814 FILING DATE: 1999-03-23	EARLIER EARLIER	
	ENCE: MBI-010	FILE	
	: Reuber, Lynne INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES	TITLE	
	Pilgrim, Jiang, C		
	Yu, Gud Ratclii		
	: Samaha, Raymond : Zhang, James		
	: Keddie, James		
	Broun, Pierre		
	FORMATION:		
	12, Application US/09533029 6664446	; Sequence 112, Appl ; Patent No. 6664446	
	9-112	RESULT 3 US-09-533-029-	a =
	4 L 224	Db 224	п
	2 L 212	Qy 212	_
223	4 LFSTSPSTSEVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKET	Db 164	_
211	SASASVCAKEESSFTSASEE	Qу 181	_
163	O QPAKPKTSNKKKGTKPKSESVITSSNSTRSESELADSSNPSGES	Db 120	п

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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
ITILE OF INVENTION: Compositions and Methods for the
ITILE OF INVENTION: Mcdification of Gene Transcription
FILE REFERENCE: 11000.1025C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pinus r
US-09-640-211A-1110
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                                                                                                                                                                                                                                                           US-09-640-211A-2258
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GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Wood, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2161
                                                                                                                                                                                                                Sequence 2258, App
Patent No. 6833446
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atch 40.0%; Score 547.5; DB 2; cal Similarity 64.4%; Pred. No. 7.8e-49; 105; Conservative 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                        117
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                                                                                                                                                                                                                                                                                                                                                        ------ARMKADSVAVDAQP-TPASSLASSTTE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKPDIKRGNFSPEEEDQIIKLHELIGNRWSTIASYLPGRTDNEIKNVWNTHLKKRL----
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                                                                                                                                                                                                                                      Application US/09640211A
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US-09-533-029-68
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for V
SEQ ID NO 2258
LENGTH: 412
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: G659 US-09-533-029-68
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
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NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 68
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 68, Apprix
                                                                                                                                                                                                                                                      Query Match 37.0%; Score 506.5; DB 2; Best Local Similarity 39.9%; Pred. No. 4.7e-44; Matches 113; Conservative 36; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yu, Ğuo-Liang
APPLICANT: Ratcliffe, Oliver
APPLICANT: pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
149 PPASPERSASSSVTESSMASSVAEEHGNAGISSASASVCAKEESSFTSASEEFQIDD---
                                    124 WSKIASQLPGRTDNEIKNVWHTHLKKRL------AQSSG-----TADEPASPCSS
                                                                                                        93;
                                                           89 WSAJAARLPGRTDNEIKNVWHTHLKKRLDAPAQGGHVAASGGKKHKKPKSAKKPAAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YLRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLRPDIKRGQFSFEEEQTIIELHAVLGNKWSTIAGHLPGRTDNEIKNYWNTHLKKRL 117
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||| |||| :||| ||||||| || || 60
1 MGRTPCCEKNIGLKKGPWTPEEDQKLIDYIQSHGHGSWRALPKRAGLLRCGKSCRLRWIN 60
                                                                                                                                                                               Similarity
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Pred. No. 1.4e-45;
9; Mismatches 14
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                                                                                                                                                                                                                                                                                           Length 327;
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                                                                                                                                                                                                                                                          77;
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                     63
   205
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; Sequence 2, Application US/09453387A
; Patent No. 6828476
; GENERAL INFORMATION:
; APPLICANT: Wilkins, Thea A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Cotton Transcription Factors and Their
; FILE REFERENCE: 023070-095600US
; CURRENT APPLICATION NUMBER: US/09/453,387A
; CURRENT FILLING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 26
; NUMBER OF SEQ ID NOS: 26
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APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Anthew
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Composition of Gene Tra
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2259
LENGTH: 391
TYPE: PRT
ORGANISM: Pinus radiata
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US-09-640-211A-2259
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                                                                                                                                                                                                                                                                                                             RESULT 9
             SEQ ID NO 2
LENGTH: 294
TYPE: PRT
ORGANISM: Gossypium hirsutum
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.7%; Score 502; DB 2;
41.9%; Pred. No. 1.8e-43;
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US-09-640-211A-2261
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Sequence 2261, Application US/09640211A PATENT NO. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
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; TYPE: PRT ; ORGANISM: Pinus radiata US-09-640-211A-2277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcriptic FILE REFERENCE: 11000-1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2277
LENGTH: 225
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Matches
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Best Local Similarity
Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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176
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                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                       LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
                                                                                                                                                                                                                                                                                           MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
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                                       SVAEEHGNAGIS 180
                                                                                    LDPQTHRPLGQPNNTP--VTRPVLEHEIPAFQNPATPEIADLLQHHRLESSPI---KPAA
                                                                                                                              QGGHVAASGGKKHKKPKSAKKPAAAAAAP----PASPE-----RSASSSVTESSMAS 168
                                                                                                                                                                           LRPDLKRGSFTEEEDELIIKLHSFVGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLSKG
                                                                                                                                                                                                                                                                  MGRSPCCEKAHTNKGAWTKQEDDRLIAHIRAHGEGGWRSLPKAAGLLRCGKSCRLRWINY
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SDAEEHPDLNLN
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                                                                                                                                                                                                                                                                                                                                                                           36.2%; Score 495.5; DB 2
50.5%; Pred. No. 3.7e-43;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2110
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2110
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US-09-640-211A-2110
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2261
LENGTH: 255
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
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Best Local :
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021ClU
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121 HKPKNDALVSSDG-----QSKSAAK 140
                                    117 DAPAQGGHVAASGGKKHKKPKSAKK 141
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                                                                                                KRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKKL-----
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                                                                           KRGKFSLQEEQTIIQLHALLGNRWSAIATHLPKRTDNEIKNYWNTHLKKRLAKMGIDPVT
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                          36.0%; Score 493; DB 2;
64.1%; Pred. No. 3.6e-43;
tive 14; Mismatches 24
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; LENGTH: 302;
; TYPE: PRT
; ORCANISM: Gossypium hirsutum
US-09-453-387A-6
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US-09-453-387A-6
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; ORGANISM: Eucalyptus
US-09-640-211A-2201
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US-09-640-211A-2201
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APPLICANT: Wilkins, Thea A.
APPLICANT: The Regents of the University of Californi
APPLICANT: The Regents of the University of Californi
TITLE OF INVENTION: Cotton Transcription Factors and T
FILE REFERENCE: 023070-095600US
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2201
LENGTH: 171
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                                                                                                                                                                                                                                                                                         Matches 112;
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CURRENT FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
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Similarity 41.3%; Pred. No. 3.1e-42;
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                                                          QKSPAAPS-----KNPEAARRGTAGNGNTNGNGSGSSSTHVVRTRATRCSKVFINPPHYT 174
                                                                                               QGGHVAASGGKKHKKPKSAKKPAAAAAPPASPERSASSSVTESSMA-------
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US-09-640-211A-872

US-09-640-211A-872

Sequence 872, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOCTWARE: FSatSEQ for Windows Version 4.0
SEQ ID NO 872
LENGTH: 102
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-640-211A-872
Search completed: June 24, 2006, 00:05:31 Job time : 51 secs
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2: uniprot_trembl:*
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Biocceleration Ltd.
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  O7xbh4 oryza sativ O6x77 triticum ae O96463 hordeum vul O6k186 oryza sativ O2993 petunia hyb O04108 oryza sativ O7xdc7 oryza sativ O7xdc7 oryza sativ O9slt nicotiana t O9slt nicotiana t O9slt nicotiana t O9slt nicotiana t O9slt nicotiana t O9slt nicotiana t O9slt signification max P93391 nicotiana t O9xius glycine max O9ltc4 arabidopsis O9xius Glycine max O9ltc4 arabidopsis O9xius Glycine max O9ltc4 arabidopsis O9xius Glycine max O9ltc9 arabidopsis O9xius Glycine max O49744 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis O9ltc9 arabidopsis
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Osnato M., Mattana M., Baldoni E., Coraggio I.;

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Q6IX77
ID Q1
AC Q1
DT 01
DT 01
DT 01
OT 01
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                                                                                                           RESULT
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Best Local S
Matches 257
SULT 2
QGIX77 WHEAT PRELIMINARY; PI
QGIX77; WHEAT PRELIMINARY; PI
QGIX77;
05-JUL-2004, integrated into Un
05-JUL-2006, sequence version 1
07-FEB-2006, entry version 18.
Transcription factor Myb2.
Name=Myb2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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DNA_BIND
CONFLICT
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Plant J.
-!- FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y11414; CAA72217.1; -; mRNA.
EMBL; AY333484; AAP92750.1; -; mRNA.
EMBL; AL731616; CAE05446.2; -; Genomic_DNA.
EMBL; AF467733; AAL78372.1; ALT_FRAME; mRNA.
PIR; T03825; T03825.
HSSP; P06876; IGV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50090; MYE DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00249; Myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; Q7XBH4; -.
InterPro; IPR001005; Myb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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-i- FUNCTION: Putative transcription factor which is may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in cold stress response.
SUBCELLULAR LOCATION: Nucleus (Probable).
INDUCTION: By cold stress.
MISCELLANEOUS: Arabidopsis plants overexpressing MYB4 sl
phenotype and increased tolerance to cold and freezing.
SIMILARITY: Contains 2 Myb DNA-binding domains.
CAUTION: Ref.4 sequence differs from that shown due to frameshift in position 138.
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; ps00334; MYB_2; 1.
; ps50090; MYB_3; 2.
; ps50090; MYB_3; 2.
iding; Nuclear protein; 1
257 M
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                                                                                                                                                                                                                                                                                                                           LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA
                                                                                                                                                                                                                      SASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSMEPGDAFVAPPSADDMDY
                                                                                                                                                                                                                                                                         QCGHVAASGGKKHKKPKSAKKPAAAAAAPPASPEBSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                                                                                                                                                                            LRPDIKRGNFSKEEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA
                                                                                                                                                                                                                                                                                                                                                               MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                                                                                                                                             MGRAPCCEKMGLKKGPWTPEEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY
                                                                                                                                                                                                                                                        QGGHVAASGGKKHKKPKSAKKPAAAAAAPPASPERSASSSVTESSMASSVAEEHGNAGIS
                                                                                                                                                  WLGVFMESGEAQDLPQI
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                                                                                                                                                                                                     SASASVCAKEESSFTSASEEFQIDDSFWSETLSMPLDGYDVSMEPGDAFVAPPSADDMDY
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257 AA;
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62
138
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                                                      integrated into UniProtKB/TrEMBL
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27914
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112
159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in; Transcription; Transcription re 
Myb-related protein Myb4.

/FTId=PRO_0000197080.

Myb 1.

Myb 2.

SAKKPAAAAAAPPASPERSASS -> TRRSQI
ERSARRR (in Ref. 4).
S -> L (in Ref. 2).
S -> L (in Ref. 2).
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                                                                                  PRT;
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RESULT 3

Q96463 HORVU

Q96463;
AC

Q96463;
DT

Q1-FEB-1997, integrated into UniProtKB/TrEMBL.
DT

Q1-FEB-2006, entry version 1.
DT

Q7-FEB-2006, entry version 32.
DE

Myb4 transcription factor (Fragment).

GN

Name=myb4;
CS

Hordeum vulgare (Barley).
OS

Hordeum vulgare (Barley).
CC

Eukaryota; Viridiplantae; Streptophyta; Embryophy
CS

Spermatophyta; Magnoliophyta; Liliopsida; Poales;
CC

NCBI_TaxID=4513;
RN

CTISSUE=Endosperm;
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR01005; Myb DNA bd.
Pfam; PF00249; Myb DNA-bInding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00034; MYB_2; 1.
PROSITE; PS00034; MYB_2; 1.
DNA-binding; Nuclear protein; Repeat.
DNA-binding; Nuclear protein; Repeat.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:00045449; P:regulation of transcription;
GO; GO:0045449; P:regulation of transcription;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacese; BEP clade;
Pooidese; Triticese; Triticum.
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HSSP; Q03237; 1A5J.
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Seed;
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Pred. No. 4.9e-61;
6; Mismatches 43
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                                                                                                                                                                                    Embryophyta; Tracheophyta;
                                                                                                                                                               Poales;
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IE
GO; GO:0045449; P:regulation of transcription; IE
InterPro; IPR011287; Homeodomain-rel.
InterPro; IPR011287; Homeodomain-rel.
InterPro; IPR001287; Homeodomain-rel.
InterPro; IPR001287; Homeodomain-rel.
InterPro; IPR001287; Homeodomain-rel.
INTERPRO249; Myb_DNA-bInding; 2.
SWART; SW00717; SANT; 2.
SWART; SW00717; SANT; 2.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS00334; MYB_3; 2.
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SEQUENCE 288 AA; 31044 MW; 4C0EE58A9C5F7D38 C
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Q6K1SG;
Q6K1SG;
Q5-JUL-2004, integrated into
Q5-JUL-2004, sequence versior
Q7-FEB-2006, entry version 1(
Putative myb protein.
Name-B1215B7.15;
                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
            Copyrighted Distributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed under the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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            by the UniProt Consortium, under the Creative Commons
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            see http://www.uniprot.org/terms Attribution-NoDerivs License
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8.7e-54;
47;
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a; Poales; Poaceae; BEP cla
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R EMBL; APDOUSSE,

JR HSSP; Q03237; 1A5J.

JR Gramene; Q6K1S6; ---

DR GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:00045449; P:regulation of transcription; IEA

InterPro; IPR012287; Homeodomain-rel.

DR InterPro; IPR012287; Homeodomain-rel.

DR InterPro; IPR010287; HOMEODOMA; Dod.

Pfam; PF00249; Myb DNA-binding; 2.

SMART; SM00717; SANT; 2.

DR PROSITE; PS00031; MYB 2; 1.

DR PROSITE; PS00031; MYB 2; 1.

DR PROSITE; PS00034; MYB 2; 1.

DR PROSITE; PS00034; MYB 3; 2.

KW DNA-binding; Nuclear protein; Repeat.

PROSITE; PS00034; MYB 3; 2.

NW DNA-binding; Nuclear protein; Repeat.

SEQUENCE 258 AA; 28469 MW; 61FDBC1C586612E'

SEQUENCE 258 AA; 28469 MW; 61FDBC1C586612E'
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Q02993;
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Bukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
asterids; lamiids; Solanales;
NCBI_TaxID=4102;
                                                     EMBL;
                                                                                                                                                                 MEDLINE=94035159; PubMed=8220462;
Avila J., Nieto C., Canas L., Beni
"Petunia hybrida genes related to
                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=v26; TISSUE=Floral;
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996,
07-FEB-2006,
            HSSP; P06876; 1GV2.
TRANSFAC; T02890; -
                                                                                  Copyrighted
Distributed
                                                                                                                           animal myb proto-oncogenes.";
Plant J. 3:553-562(1993).
-!- SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                  Name=myb.Ph2;
                                                                                                                                                                                                                                                                                                                                                  Protein
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PETHY
                                       S26604; S26604.
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                                                                                                                                                                                                                                                                                                                                                                                            integrated
                                                     CAA78387.1;
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C:nucleus;
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IEA.
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GO; GO:0045449; P:regulation of transcription; IEA.
RINEETPTO; IPR011287; Homeodomain-rel.
RINEETPTO; IPR01105; Myb_DNA_bd.
R Pfam; PF00249; Myb_DNA-binding; 2.
RPART; SMO0717; SANT; 2.
RPCSITE; PS00037; MYB 1; UNKNOWN_1.
RPCSITE; PS00034; MYB 2; L.
RPCSITE; PS00034; MYB 2; L.
RPCSITE; PS00034; MYB 3; 2.
RPCSITE; PS00034; MYB 3; 2.
RPCSITE; PS00030; MYB 3; 2.
RPCSITE; PS00034; MYB 2; L.
RPCSITE; PS00034; MYB 3; 2.
RPCSITE; PS00034; MYB 2; L.
RPCSITE; PS00034; MYB 3; 2.
RPCSITE; PS00034; MYB 3; 2.
                                                                                                                                                                                                                                                                                      Myb factor.

Name=myb; Synonyms=OSJNBa0055P24.4;

Name=myb; Synonyms=OSJNBa0055P24.4;

Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; BEP clade;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                          Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T. Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                        Buell R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                             (er) Plant Gene Regi
[2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
TISSUE-Coleoptiles;
MEDLINE-97375319; PubMed-9235602;
Lu Y.-P., Zhen R.-G., Rea P.A.;
FALPT4; a fourth member of the Arabidopsis phosphate transporter
                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2006,
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01-JUL-1997,
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O04108;
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Pred. No. 1.9
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Q7XDC7 OYSA
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D7 01-OCT-2
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Best Local S
Matches 150
EMBL; AE016959; AAP5428
HSSP; P06876; 1GV2.
Gramene; Q7XDC7; -.
G0; GO:0005634; C:nucle
G0; GO:0003677; F:DNA b
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01-OCT-2003,
01-OCT-2003,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                          Myb factor.

ORFNames=LOC Os10g33810;

ORFNames=LOC Os10g33810;

Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein; Repea
SEQUENCE 276 AA; 30065 MW; 4503
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription;
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR0101005; Myb_DNA_bd.
Pfam; PF00249; Myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan O.,

Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC037425; AAG13574.1; -; PIR; T03823; T03823. HSSP; P06876; 1GV2.
                                                                                                                                           Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gramene;
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                                                                                               AAP54284.1;
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30065 MW; 45037ADE5557CF25
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    binding;
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Pred. No. 1.4e-43;
4; Mismatches 61;
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Attribution-NoDerivs License
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Best Local S
Matches 150
                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                           MEDLINE-21066940; PubMed=11148294; DOI=10.1105/tp Sugimoto K., Takeda S., Hirochika H.; "MYB-related transcription factor NtWYB2 induced elicitors is a regulator of the tobacco retrotran defense-related genes."; plant Cell 12:2511-2528 (2000).
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InterPro; IPR012087; Myb DNA bd.
Pfam; PF00249; Myb DNA-bInding; 2.
SMART; SM00717; SANT; 2.
SMART; SM00717; SANT; 2.
INKNOWN 1.
PROSITE; PS00034; MYB 1; UNKNOWN 1.
PROSITE; PS00034; MYB 2; UNKNOWN 1.
PROSITE; PS50099; MYB 3; 2.
DNA-binding; Nuclear protein; Repeat.
SEQUENCE 276 AA; 30065 MW; 45037ADE5557CF25 CRC64;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
GO; GO:0045449; F:regulation of transcription;
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR0101005; Myb DNA bd.
Pfam; PF00249; Myb DNA-bd.
SMART; SM00717; SANT; 2.
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01-MAY-2000, sequence version
07-FEB-2006, entry version 30
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                                                                                                                                                                                                                          AB028652; BAA88224.1; -; mRNA.
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Best Local :
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IE;
GO; GO:0045449; P:regulation of transcription; IE;
InterPro; IPR011287; Homeodomain-rel.
InterPro; IPR00105; Myb_DNA_bd.
Pfam; PF00249; Myb_DNA_bInding; 2.
SMART; SM00717; SANT; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00037; MYB_2; 1.
PROSITE; PS000309; MYB_3; 2.
DNA-binding; Nuclear Protein; Repeat.
SEQUENCE 281 AA; 31985 MW; 0EB07C4900A5522A CI
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PROSITE; PS00334; MYB_2; 1
PROSITE; PS50090; MYB_3; 2
PNA-binding; Nuclear proce
SEQUENCE 281 AA; 32029
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JT2 TOBAC
Q9SLT2 TOBAC
Q9SLT2;
Q9SLT2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugimoto K., Takeda S., Hirochika H.;
"MYB-related transcription factor NtMYB2 induced by wounding elicitors is a regulator of the tobacco retrotransposon Ttol defense-related genes";
Plant Cell 12:2511-2528(2000).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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07-FEB-2006, entry version 29.
Myb-related transcription factor LBM1.
                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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Sugimoto K., Takeda S., Hirochika H.;
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Pred. No. 2
       Repeat.
0EB07C4900A5522A CRC64;
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Best Local S
Matches 147
TRANSFAC; T028/3,
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription;
InterPro; IPR012287; Homeodomain-rel.
TnterPro; IPR001005; Myb_DNA_bd.
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74 LYCES
Q40174 LYCES
Q40174;
                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of a myb-related cD (Accession No. x98308) (PGR96-060)."; Plant Physiol. 0,0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hypocotyl;
MEDLINE=96270378; PubMed=8639738;
Lin Q., Hamilton W.D.O., Merryweather A.;
"Cloning and initial characterization of 14 myb-related comato (Lycopersicon esculentum, cv Ailsa Craig).";
Plant Mol. Biol. 30:1009-1020(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato).

Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996, integrated into UniProtKB/TrEMBL 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 37.
                                                                                                                                                              EMBL; X98308; CAA66952.1;
PIR; T07395; T07395.
HSSP; P06876; 1MBK.
TRANSFAC; T02873; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THM18 protein. Name=THM18;
                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TMHT
                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Hypocotyl;
Lin Q., Hamilton W.D.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --NYQPPQNSKRHSKNNLDSKAPSTSQTFNNSDNFSNIQEDINGPVTGPNSPQRSSSEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGHVAASGGKKHKKPK-SAKKPAAA------AAAPPASPERSAS--S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVRAPCCEKMGLKKGPWTPEEDQILVSYIQTNGHGNWRALPKLAGLLRCGKSCRLRWTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMPLDGYDVSME--PGDAFVAPPSA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.4%; Score 690; DE
48.8%; Pred. No. 5.2e
tive 35; Mismatches
                                                                                                                                                                                                                                              mRNA
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.2e-43;
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RESULT 11

QSSLT1_TOBAC

JOSUT1_TOBAC

AC QSSLT1_TOBAC

AC NAMPB-TOBAC

AC NAMB-TAMB-TOBAC

AC MEDLLNE=210665

AC MEDLLOE IS

AC MEDLLOE

AC MEDL
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Best Local Similarity
Matches 143; Conserv
EMBL; AB028650; BAA88222.1; -; mRNA.
HSSP; P06876; IGV2.
TRANSFAC; T05249; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
GO; GO:003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcr
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR001005; Myb DNA bd.
Pfam; PF00249; Myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00033; MYB-2; 1.
PROSITE; PS00033; MYB-2; 1.
PROSITE; PS00033; MYB-3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00249; Myb_DNA-binding; 2.
SMART; SM0717; SANT; 2.
PROSITE; PS00037; MYB 1; UNKNOWN 1.
PROSITE; PS00334; MYB-2; 1.
PROSITE; PS00334; MYB-3; 2.
DNA-binding; Nuclear protein; Repeat.
DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=21066940; PubMed=11148294;
Sugimoto K., Takeda S., Hirochika F
"MYB-related transcription factor P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core ex
spermatos; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4097;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                               see http://www.uniprot.org/to
Attribution-NoDerivs License
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eudicotyledons;
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Query Match
Best Local S
Matches 138
                                                                                                                                       HSSP; P06876; IGVD.
GO; GO:0005634; CINUCleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IE.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR012087; Myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS000337; MYB 1; UNKNOWN_1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS000334; MYB 3; 2.
PROSITE; PS000344; MYB 3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000, integrated into UniProtKB/TrEMBL. 01-MAY-2000, sequence version 1. 07-FEB-2006, entry version 27.
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SEQUENCE 277 AA; 32076 MW; D4F3DFB2B1252885 CRC64;
                                                                                                  DNA-binding; Nuclear SEQUENCE 264 AA; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akada S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu
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138; Conserv
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AB029159; BAA81730.1; -; Genomic_DNA.
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                                                                                             protein; Repeat.
30387 MW; A2B710A0FECAE66A CRC64;
                    49.5%;
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     39;
Score 677.5;
Pred. No. 4.1e
39; Mismatches
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Pred. No. 1.4e-42;
Pred. No. 1.5e-42;
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4.1e-42;
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EMBL; AB028651; BAA88:
PIR; T03850; T03850.
HSSP; P06876; 1MBK.
                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription;
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR001005; Myb DNA bd.
Pfam; PF00249; Myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
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Yang, Y, Klessig D.F.;
Submitted (SEP-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor Myb1 (Myb-related transcription Name=myb1; Syrnonyms=lbm3; Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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                                   PROSITE; PS00334; MYB_2; PROSITE; PS50090; MYB_3;
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MEDLINE=97121500; PubMed=8962166; DOI=10.1073/pnas.93.25.14972;
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AB028651; BAA88223.1;
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T05250; -.
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Acad. Sci. U.S.A.
       Nuclear
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PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein; Repeat.
DNA-binding; Nuclear protein; Repeat.
SEQUENCE 264 AA; 30201 MW; ADF2B192ABB63780 CRC64;
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GO; GO:0045449; F:regulation of tran.
InterPro; IPR012287; Homeodomain-rel
InterPro; IPR01005; Myb_DNA_bd.
Pfam; PF00249; Myb_DNA_binding; 2.
SMART; SM00717; SANT; 2.
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NUCLEOTIDE SEQUENCE.

Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.

Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Cishi K., Ko

Narusaka M., Shin-i T., Nakagawa M., Sakumoto N., Oishi K., Ko

Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiye

Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,

Hayashizaki Y., Shinozaki K.;

"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL)

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=20277480; PubMed=10819329; DOI=10.1093/dnares/7.2.131;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata i
"Structural analysis of Arabidopsis thaliana chromosome 3. I. i
features of the regions of 4,504,864 bp covered by sixty Pl and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000, sequence version 1.
07-FEB-2006, entry version 29.
Myb-related transcription factor (MYB
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AB025608; BAA95738.1; -; G
AYS50296; AAS58507.1; -; m
AK176617; BAD44380.1; -; m
AK176693; BAD44456.1; -; m
AR176693; BAD44456.1; -; m
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EMBL/GenBank/DDBJ databases
                             ; Genomic_DNA.
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                                                                                                                                                             Commons
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR012287; Homeodomain-rel.
Ffam; PF00249; Myb_DNA-bInding; 2.
SMART; SM00717; SANT; 2.
SMART; SM00717; SANT; 2.
RPROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
RPROSITE; PS00037; MYB_3; 2.
RPROSITE; PS00037; MYB_3; 2.
RPROSITE; PS00037; MYB_3; 2.
SMONA-binding; Nuclear Protein; Repeat.
SEQUENCE 285 AA; 32042 MW; SICEF6C6DF50F828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.4%; Score 661.5; DB 2; Length 285; Best Local Similarity 49.0%; Pred. No. 6.9e-41; Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps
                                                                                                                                                                                                                              120 QPAKPKTSNKKKGTKPKS-----ESVITSSNSTRSESELADS----SNPSGES 163
                                                                         224 LYSQDEHNYVSNDLEVAGLVEIQQEFQNLGSANNEMIFDSEMDFWFDVLARTGGEQDL 281
                                                                                                                                                     164 LFSTSPSTSEVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKET 223
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